OM nucleic - nucleic search, using sw model

GenCore version 4.5
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Run on: November 29, 2001, 08:52:45 ; Search time 10554.9 Seconds
(without alignments)
10137.587 Million cell updates/sec

Title: US-09-526-329-40
Perfect score: 6486
Sequence: 1 tcctcctcctccctcctc..........ggtccattcaagcaggac 6486

Scoring table: IDENTITY_NUC
GapOp 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
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9: gb_pr:*
10: gb_ro:*
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12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: gb_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_om:*
20: em_or:*
21: em_ov:*
22: em_pat:*
23: em_ph:*
24: em_pl:*
25: em_ro:*
26: em_sts:*
27: em_sy:*
28: em_un:*
29: em_vi:*
30: em_hgo_hum:*
31: em_hgo_inv:*
32: em_hgo_rod:*
33: em_htg_hum:*
34: em_htg_inv:*
35: em_htg_rod:*
36: em_htg_other:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.		Score	Query Match Length	DB	ID	Description
1		6485	100.0	6486	9	AF110465	Homo sapi
2		6443.8	99.3	166308	9	CN50IDX2	Human chr
3		6389.4	98.5	210791	9	CN50IDV7	Human chr
4		1633.4	25.2	1717	9	AB025272S3	Homo sapi
5		1338.4	20.6	1722	9	AB018563	Homo sapi
6		701.2	10.8	1152	9	AF110466	Homo sapi
7		701.2	10.8	3144	9	AB035343	Homo sapi
8		701.2	10.8	3240	9	AB035342	Homo sapi
9		701.2	10.8	3532	9	AB035341	Homo sapi
10		701.2	10.8	3599	9	AB035340	Homo sapi
11		699.2	10.8	1177	9	AF137027	Homo sapi
12		644.4	9.9	753	9	AB025273	Homo sapi
13		570.4	8.9	627	9	AB025272S2	Homo sapi
14	c	506	7.8	110879	9	AB025272S1	Homo sapi
15	c	506	7.8	114438	9	AC016603	Homo sapi
16	c	506	7.8	204843	9	AC010356	Homo sapi
17		497.6	7.7	1248	9	AC010359	Homo sapi
18		493.8	7.6	137808	9	AF110467	Homo sapi
19		490	7.6	155145	9	AC008889	Homo sapi
20	c	478.6	7.4	174095	9	AL360013	Homo sapi
21		474.8	7.3	172757	9	AL356788	Homo sapi
22		472	7.3	173185	9	AC091127	Homo sapi
23	c	467.4	7.2	186497	9	AC011476	Homo sapi
24		467.2	7.2	192876	9	AP003531	Homo sapi
25	c	466.4	7.2	145442	9	AC004859	Homo sapi
26		466	7.2	120766	9	AC004150	Homo sapi
27	c	463	7.1	224400	9	AC008758	Homo sapi
28		462.6	7.1	100732	9	AL133347	Human DNA
29	c	462.2	7.1	150036	9	AP000557	Homo sapi
30		462	7.1	169997	9	AC008440	Homo sapi
31		460.8	7.1	206836	9	AC011501	Homo sapi
32		459	7.0	171523	9	AC021616	Homo sapi
33	c	457.2	7.0	211544	9	AC025165	Homo sapi
34		456	7.0	145631	9	AC090114	Homo sapi
35		454.8	7.0	169237	9	AC009516	Homo sapi
36		454.8	7.0	176051	9	AC023490	Homo sapi
37		454.6	7.0	212656	9	AC007957	Homo sapi
38		454.4	7.0	149618	9	AP000556	Homo sapi
39		454.4	7.0	157086	9	AC084291	Homo sapi
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41	c	448.4	6.9	212656	2	AC007957	Homo sapi
42	c	446.6	6.9	199287	2	AC023157	Homo sapi
43	c	444.6	6.8	157756	9	AC007003	Homo sapi
44	c	444	6.8	97078	2	AC005841	Homo sapi
45	c	443.6	6.8	172800	2	AL356597	Homo sapi

RESULT 1
AF110465
LOCUS   AF110465   6486 bp   DNA   PRI   18-MAR-1999
DEFINITION Homo sapiens T-cell leukemia/lymphoma 1B (TCL1B) gene, complete
cds.
ACCESSION   AF110465
VERSION   AF110465.1 GI:4324702
KEYWORDS   .
SOURCE   human.
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 6486)
AUTHORS   Pekarsky,Y., Hallas,C., Isobe,M., Russo,G. and Croce,C.M.
TITLE   Abnormalities at 14q32.1 in T cell malignancies involve two
oncogenes
JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 96 (6), 2949-2951 (1999)
MEDLINE   99178995
REFERENCE   2 (bases 1 to 6486)
AUTHORS   Pekarsky,Y., Hallas,C. and Croce,C.M.

ALIGNMENTS

8

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TITLE
JOURNAL   Direct Submission
          Submitted (02-DEC-1998) KCI, Thomas Jefferson University, 233 South
          10th Str. BLSB 1032, Philadelphia, PA 19107, USA
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /chromosome="14"
                     /map="14q32.1"
     mRNA            join(141..329,4439..4609,4971..5039,5634..6330)
                     /gene="TCL1B"
     gene            141..6330
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     CDS             join(168..329,4439..4609,4971..5024)
                     /gene="TCL1B"
                     /codon_start=1
                     /product="T-cell leukemia/lymphoma 1B"
                     /protein_id="AAD16996.1"
                     /db_xref="GI:4324703"
                     /translation="MASEASVRLGVPGRLWIQRGIXEDEEGRTWTVVVRENPSRR
                     EWARASQGSRYEPSITVHLMQMAVHTRELLSSGQMPFSQLPAWWQLIPGRKYRAADSS
                     FWEIADHGQIDSMEQLVLIYQPERKD"

BASE COUNT     1600 a   1559 c   1687 g   1639 t      1 others
ORIGIN
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Best Local Similarity   100.0%;   Pred. No. 0;
Matches 6486;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy      1 tcctcctcccctcccctcctccccgacctgcaccgacccccactgccgccccccccac   60
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Qy     61 tgccggccggcccgggcccccacccacgccggagcctgctccattaaggaggagctga  120
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Qy    121 aagctacacgtgtagacctagaagagcgggtcccggttgcagaactggccatggccgag  180
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Db    121 AAGCTACACGTGTAGACCTAGAGGCGGGTCCCGGTTGCAGAACTTGCCATGGCCTCCGAG  180

Qy    181 ctttctgttgcgtcttagggttgtcccccctggccgtctctgtgatccagaagcgtcacg  240
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Db    181 CTTTCTGTTGCGTCTTAGGGTTGTCCCCCTGGCCGTCTCTGTGATCCAGAGGCGTCACG  240

Qy    241 aagatgagggagggaggaaacctgggtgactgtgtcgttcgttcaatccctcgcgtaggg  300
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Qy    301 aatggccagggcccctcccagggcagcagagtgagtcctgggcacgagaggggggctgtggg  360
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Qy    361 gagggctgcgcactgacccctgcccgttgtgggaccggtgggggtcagagggggccgtt  420
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Qy    421 ctcaccgcactggaaaactcacttctgtgcagttctaggagcgcagcaatgtccatgcc  480
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Db    721 CCTGGAGGGCACCCAGGTGGGCCAACAGGTGGGCCAACAGGGATGAAACATGACATTGGTCGTCAGATTTACTGATCT  780

Qy    781 gcaaaatgaggaataataccctctgtgccaagctagtcacagaacatgtcacacatatgg  840
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Db    841 CTCACCGCCTGAATGGCCTGGGGAAGCAATTTGACTGATAACAGATTCTGGAAATTAATTC  900

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Qy   1021 gaagtaaaatacacagctaggcgtcttcgtgttggggtcggttggtgggggaattgaattcccaggacacga  1080
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   3061 ATGGATTCTTCAAATAACTTAGCCACAGGGTGGGGATAAGGGAACTTACTTAGTAAGTATTTTT 3120

Qy   3121 ttcccctttctttcttaaaaataggatcgatgtcttaggtggggaatttccccggg 3180
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Db   3121 TTCCCCTTCTTTCTTAAAAAATAGATCGATGTCTTAGGGTGGGAATTAGGCTTCCTGGGCG 3180

Qy   3181 acacatcttaatgcaaagatcagccaccctttctctgtaaaggtgtggtaaacatttt 3240
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Db   3181 ACACATCTTAATGCAAAGATCAGCCACCTTTCTCTGTAAAGGTCTGGGAATAGGCTTTCCTGGGCG 3240

Qy   3241 ccacttgagagctatgctcttgcagtctacctcagctctgctattggcagtgcaaagcagct 3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 CCACTTGAGAGCTATGCTCTTGCAGTCTACCTCAGCTCCTATTGCAGTGCAAAGCAGCT 3300

Qy   3301 aaaggccaacgtaaagtaaaggaatggcgcggaaggaggggcgcctagttcttattatttatt 3360
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Qy   3361 tgcaaaagcagatgcaagccagacttagttcgtgatcctgaatctcagatcagaataca 3420
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Qy   3421 cagagaagggagagagatttgcccgtatataattaaaatactctctttgcaaagagcagtccat 3480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 CAGAGAAGGAGAGAGATTTGCCGTATAATTTAAAATACTTCTCTTTGCAAAAGCAGTCCAT 3480

Qy   3481 aaaaaaagtgaagcaacaaactgagaaaaattattcaacacatgctctgattgatagagc 3540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 AAAAAAAGTGAGGCAACAAACTGAGAAAAATTATTCAACACATGTCTGATTGATAGAGC 3540

Qy   3541 actaaatatttcttaattcacaaaagacatttttatcccaaaagaagaagaatacttagaaaat 3600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 ACTAATATTCTTAATTCACAAAAGACATTTTATCTCACAAAGAAGAACAAATACTTAGAAAAT 3600

Qy   3601 tgtgcaaaagactttccatttgttgcataacgtaggaagcttggttttactttttccta 3660
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Db   3601 TGTGCAAAAGACTTTCCATTTGTTGCATAACGTAGGAAGCTTGGTTTTACTTTTCCTA 3660

Qy   3661 tcatcttttctaaacttccagtaccagcctaatttgtattttattatttatgtattatt 3720
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Qy   3721 ttgagacagagtcttgctctgtcctcccaggctgagtgcagtgacctgacgatagcttac 3780
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Db   3721 TTGAGACAGAGTCTTGCTCTGTCTCCCAGGCTGGAGTGCAGTGACGCGATAGCTTAC 3780

Qy   3781 aacagccttacctcccaggttcaagagaatcttcacctagctccgagtagctggg 3840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3781 AACAGCCTTCACCTCCCAGGTTCAAGAAAATCTTCTCACCTAGCTTCCCGAGTAGCTGG 3840

Qy   3841 actgtaggcacatgccaccacatggcccagctaattttttttttttttgtagagacagagtctc 3900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841 ACTGTAGGCACATGCCACCACACCGGCCTAATTTTTTTTTATTTTTGTAGAGACAGAGTCTC 3900

Qy   3901 attatgttgccaggctggtcttcnagactcgtggacctggctcnagcagtcctcctgccttggcct 3960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

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Db   3901 ATTATGTTGCCAGACGTAGTCTTGAACTCGTGGCTTCTCCTGGCCTT 3960
                                                      
Qy   3361 cccaaagtgttgggattacagggcataagccacttgcctcccagccttattcgtatattac 4020
          ||||||    |||||||||      ||||||||       |||||||||||||||||||||
Db   3961 CCCAAAGTGTTGGGATTACAGGCACTGCCTCCCAGCCTTATTCGTATATTTAC 4020

Qy   4021 tataagtgtgtgaagtcatgatcatgatcagaactgccatatatttgcgggaaaatctatcac 4080
          ||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4021 TATAAGTGTGTGAAGGTCATGATCAGAACTGCCATATATTTTGGCGGGAAAATCTATCAC 4080

Qy   4081 cctcagatccaggagtccatggatatctcttgttttaaaacgaagagatttaaaaaattacgg 4140
          ||||||||||||||||||||||    ||||||||       ||||||||||||||||||||
Db   4081 CCTCAGATCCAGGAGTCCATGGATATCTTGTTTTTAAAACGAAGAGATTTAAAAAAATTACGG 4140

Qy   4141 caatggcagagatggagaccccaaagaatactcagcttaacccaagtgttgacaggtt 4200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4141 CAATGGCAGAGATGGAGAGCCCCAAAGAATACTCAGCTTTAAACCCAAGTGTTGACAGGTT 4200

Qy   4201 ggaaacagtggctaaatttggggattgcaatgtggggcaggggtgcagggg 4260
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Db   4201 GGAAACAGTGGCTAAATTTGGGGATTGCAGTGTGGGGCGGCAGGGTGCAGGGG 4260

Qy   4261 gccagagaggggccccaggccatcctagataggagcccactggccagttgctccttggt 4320
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Qy   4321 ctggaattctgaaaacatttacctctgacctggccagcccactggccattgccttcttgttgc 4380
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Qy   4381 agcccagttgggacagggaaccctatccatgatttgtccgcctcttttctggtccccttcagta 4440
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Db   4381 AGCCCAGTTGGGACAGGGAAACCCTATCCATCATGATTTGCCGCCTCTTTTTCTGGTCCCCTTCAGTA 4440

Qy   4441 tgaaccagcatcacagtgcacttgtggcagatggcagtgcataccctcttggt 4500
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Db   4441 TGAACCAGCACATCACAGTGCACTTGTGGCAGATGGCAGTGCATACCCTACTCTC 4500

Qy   4501 ctccggccagatgccccttctccaagctggcacgggggcaggcttacccccgggggaa 4560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4501 CTCCGGCCAGATGCCCTTCTCCCAAGCTCCCCGTGTGGCCAGTTGCATTACCCGGGGAGCTTACTCTC 4560

Qy   4561 gtacggagcagcggattccagtttctgggaaatagcgacaggtggcccctgacctgtgtgtg 4620
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Qy   4621 gtggttctaggtgaagcgacaggtgccctggtgactgcgtgccctctctctctg 4680
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Db   4621 GTGGTTCTAGGTTGAAAGCGACAGGTGGCCCCTGGTCACTGCTGCCCTCTCTCTCTG 4680

Qy   4681 tgccctggcccccttggggtttcttgtctcctgttgctcaagtcttccttca 4740
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Db   4681 TGCCCCTGGCCCCCTTGGGGTTTCTTGTCTCCTTGTTGCTCAAGTCTTCCTTCA 4740

Qy   4741 aggaggcctggagtgtgtgtggatcgatcagtcatctgagttcccatgtgggatgcaagcag 4800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4741 AGGAGGCCTGAGTGTGTGTGGATGTCTGGGTGGGTCCATGAGTTCCCATGTGGGATGCAGGCAG 4800

Qy   4801 agtgggtgaggggaggggttgcctccctggctgggatggggatgcaggcag 4860
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4801 AGTGGGTGAGGGGAGGGGTTGCCTTCCCTGGGTCTAGGGAAATCCATAAGCTGGAGTTC 4860

Qy   4861 ccacctgcctcacccctgcctgctgctctggaagaaggttctgatgtggctcccagatgacttgcca 4920
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4861 CCACCTGCCTCACCCCTGCCTGCTGCTCTCCAGCCCTTCATGGGCGGCCGTTAAGGCCA 4920

Qy   4921 ACTGGAACGAGAGCATCTCCCAGAGGTTCTGATGGGCTGCTCCCCTCCTCCTCTG 4980
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Qy   5041 tatgttgggggccctgtcggtccggttgtaggggatcaagacgaaagtgagagagaacctctcct 5100
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Qy   5101 ctttcagaaagacggcgtggcctcctcctccctgctgttggctgagatttctcttacat 5160
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Db   5101 CTTTTCAGAAAGACGGGCGTGGCCTCCTCCTCCCTGCTCGTTTGCTGAGATTTTCTTACAT 5160

Qy   5161 agccacctgtcacctctgttcccccagccccctggaattgctggatgtgatgtacaacagtggggcc 5220
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Db   5161 AGCCACCTGTCACCTCTGTTCCCCAGCCCCTTGGAATGTGATGGTACACAGTGGGGCC 5220

Qy   5221 cccataataagttcctaaaagcatgggatctcatacgaataagatgaatcatcattaatccttg 5280
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Db   5221 CCCATAATAAGTTCCTAAAAGCATGGGATCTCATACGAATAAGACTCATCATTTAATCCTTG 5280

Qy   5281 tgagaattttgtgaggtgtaacgttgttaaatgtccatttcacgacgaataagactcatcatt 5340
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Db   5281 TGAGAATTTTGTGAGGTGTAACGTTGTTAAATGTCCCATTTCACGACGAATAAGACTCATCATT 5340

Qy   5341 gggatgggaatgactttcctgagaccatacagacgaggaaatagggtggaatcttagtgat 5400
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Db   5341 GGGGATGGGAATGACTTCCTCGAGACCATACAGCCCAGGAAATAGGCGGTGAAATCTAGTGAT 5400

Qy   5401 ctcgggtccctagatttaacatggcactgaagtgtcgtgttgacagtgccttggaggac 5460
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Db   5401 CTCGGGTCCCTAGATTTAACCATGGCACTGAAGTTGCCGTGTGTTGACAGGTGGCCTTGGAGGAC 5460

Qy   5461 ccagcactgacccatagagggtctcctccagatgggcagcagcttgacagcaggca 5520
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5461 CCAGCACTGACCCATAGAGGGCTCCTTCAGATGGGCAGCAGCTTGAGCAGGCCAGGCA 5520

Qy   5521 gggcctgggtccattggagggggctggcacttgccttttgacccagccagcgagcttgggatg 5580
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Db   5521 GGGCCTGGGTCCATTGGAGGGGGCTGGCACTTGCCTTTGACCCCACAGCGCTGGGATG 5580

Qy   5581 gggtgccgggctccccaataagtccactagtctcctttcctttggttcttctctcaggccctgc 5640
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Qy   5641 tggccctggcctcctcttgttgcacccagcgatagcctcctgcaggcaggacaggtagggccc 5700
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Qy   5701 ctgcacactcaagtttctctcgttttccttagttatacatgtcctgtcccaactcaagt 5760
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Db   5701 CCTTGCCTCTTCTGTTTTGCACACCACGATAGCCCTTTGAGTTATCAGTCCTGTCCCCAACTCAAGT 5760

Qy   5761 ctgtacttagggcagctggcctggacttcaactgggctccaggatgtgtggctgagcc 5820
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5761 CTCCACACTCAGTTTCTCTCGTTTTCCTTAGTTATACAGTCCTGTGTCCCCACTCAGGT 5820

Qy   5821 agtttcccctgctggtgcaagctgtgggttctgtttctctctgggccctcatgtgatc 5880
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Db   5821 CTGTACTTAGGGCAGCTGGCCTGGACTGGGGCCTTGGACTCCTGGTGTCCCCACTCAGGT 5880

Qy   5881 agtttccccctgctggtgcaagctgtgggttctgtttctctctgggccctcatgctgatc 5940
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Db   5881 AGTTTCCCCTGCTGGTGCAAGCTGTGGGTTCTGTTTCTCTCTGTGCCCCTCATGTGATC 5940

Qy   5941 ttctagatgccactcccaaatccccttcatacccacccaggatgtgtgcccagccagcct 6000
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Db   5941 TTCTAGATGCCACTCCCAAATCCCCTTCATACCCACCCAGGATGTGTGCCCAGCCAGCCT 6000

Qy   6001 ccagcaccccagtcagctcgtgattggaaactcacactggcagcgagtggttcggtt 6060
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Db   6001 CCAGCACCCCAGTCAGCTCGTGATTGGAAACTCACCATCGGCAGCGAGTGGTTCGGTT 6060

Qy   6061 taagggatggcattagaggaggagcccagtctggatgggacttggaatccctgtgggtatc 6120
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6061 TAAGAGAATGGCATTAGAGGAGGAGCCCCAGTCTGGATGTGGGACTTGGAATGCCCTGTGGGTATC 6120
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RESULT  2
CNS01DX2
LOCUS       CNS01DX2      163308 bp    DNA             PRI       26-APR-2001
DEFINITION  Human chromosome 14 of DNA sequence BAC R-164H13 of library RPCI-11
            from chromosome 14 of Homo sapiens (Human), complete sequence.
ACCESSION   AL139020
VERSION     AL139020.5  GI:13539193
KEYWORDS    HTG.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 163308)
  AUTHORS   Heilig,R., Petit,J.L., Vico,V., Dasilva,C., Robert,C., Wincker,P.,
            Brottier,P., Cattolico,L., Barbe,V., Pelletier,E., Artiguenave,F.,
            Levy,M., Eckenberg,R., Bruls,T., deberardinis,V., Cruaud,C.,
            Gyapay,G., Saurin,W. and Weissenbach,J.
  TITLE     Sequencing of the human chromosome 14
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 163308)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-APR-2001) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     On Apr 3, 2001 this sequence version replaced gi:12274871.
            --------------------  Genome Center
            Center: Genoscope / Centre National de Sequencage
            Center code: GS
            Web site: http://www.genoscope.cns.fr/
            Contact: SeqRef@genoscope.cns.fr
            --------------------
            The following BAC sequence is oriented from the T7 to the SP6 end.
            Upstream BAC (overlapping the T7 end) : R-1070N10
            Downstream BAC (overlapping the SP6 end) : R-185P18 (AC=AL133167)
            --------------------  Summary Statistics
            Assembly program: Phrap; version 2.0
            Quality coverage: 6.03x in Q20 bases; sum-of-contigs
            ----------------------------------------
            Overall quality chart :
            ----------------------------------------
            Range  :  bases
            0      :
            1 - 9  :  4
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FEATURES             Location/Qualifiers
Percentage of bases with a quality value >= 40 : 99 %.
     source          1..163308
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="14"
                     /clone="R-164H13"
                     /clone_lib="RPCI-11"
     STS             6803..6993
                     /note="matching EMBL:R68409
                     RHdb:RH45107
                     dbSTS:STS38175
                     Identified using the e-PCR software (G. Schuler)"
     STS             9797..10019
                     /note="matching EMBL:T96687
                     RHdb:RH45537
                     dbSTS:STS38605
                     Identified using the e-PCR software (G. Schuler)"
     STS             14657..14855
                     /note="matching EMBL:R70888
                     RHdb:RH77821
                     dbSTS:STS54563
                     Identified using the e-PCR software (G. Schuler)"
     STS             16118..16281
                     /note="matching EMBL:AA856757
                     RHdb:RH98896
                     dbSTS:STS68645
                     Identified using the e-PCR software (G. Schuler)"
     STS             46740..46885
                     /note="matching EMBL:H01982
                     RHdb:RH44550
                     dbSTS:STS37619
                     Identified using the e-PCR software (G. Schuler)"
     STS             47277..47485
                     /note="matching EMBL:X82240
                     RHdb:RH53532
                     dbSTS:STS26938
                     Identified using the e-PCR software (G. Schuler)"
BASE COUNT    46913 a  36249 c  37941 g  45205 t
ORIGIN
```

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Query Match          99.3%;  Score 6443.8;   DB 9;  Length 166308;
Best Local Similarity 99.8%;  Pred. No. 0;
Matches 6473;  Conservative 0;  Mismatches 13;  Indels 2;  Gaps 2;

Qy      1 tcctcctcctcccccccccccccccccgactggcacccccaccactgccggcccgccccac     60
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Db  22901 TCCTCCTCCTCCCCCCCCCCCCCCCCCCGACTGGCACCCCCACCACTGCCGGCCCGCCCCAC  22960

Qy     61 tgccggcccggcccccacccaccacccgggagctgctccattaaggagaattgcgaagctgga    120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  22961 TGCCGGCCCGGCCCCCACCCACCACCCGGGAGCTGCTCCATTAAGGAGAATTGCGAAGCTGGA  23020

Qy    121 aagctacacacgtgtgagcctagaagggcgggtccccggttgcagacttgccatggcctccgaag  180
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Db  23021 AAGCTACACACGTGTGAGCCTAGAAGGGCGGGTCCCCGGTTGCAGACTTGCCATGGCCTCCGAAG  23080

Qy    181 cttctgttgcgtctagggtgccccctggccctggtggatccagaggcctggcaatctacg     240
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Db  23081 CTTCTGTTGCGTCTAGGGTGCCCCCTGGCCCTGGTGGATCCAGAGGGCCTGGCCATCTACG  23140

Qy    241 aagatgagggagggagaaacctgggtgactgtgtcgtcggttcaatccctcgctaggg     300
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                          10 -  19  :        53
                          20 -  29  :       203
                          30 -  39  :       622
                          40 -  49  :      3717
                          50 -  59  :     82215
                          60 -  69  :     11927
                          70 -  79  :     27324
                          80 -  89  :     52859
                          90 -  99  :     61384

Qy   6121 agttctgctgacacctttgcccggaaatagatccagtgtgtgacgacaagcaatgtacacgga  6180
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Db   6121 AGTTCTGCTGACACTTTGGCCCGGAAATAGATCCAGTGTGTGACGACAAGCAATGTACACGGA  6180

Qy   6181 gcctccagtgagcccatctgcacagtggggagcacatgagaggagtgggtttggcctgtgttc  6240
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Db   6181 GCCTCCAGTGAGCCCATCTGCACAGTGGGGAGCACATGAGAGGAGTGGGTTTGGCCTGTGTTC  6240

Qy   6241 tgcttattcagtcttcagctcacgtcacggaaggagatgctagtccgtgaagtgacctcacagt  6300
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Db   6241 TGCTTATTCAGTCCTTCAGCTCACGTCACGGAAGGAGATGCTAGTCCGTGAAGTGACCTCACAGT  6300

Qy   6301 actggttaattaaactttattgctcactgtccactttgtgtgctgaattggagcctcctt  6360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6301 ACTGGTTAAATTAAACTTTATTGCTCACTGTCCACTTTGTGTGCTGAATTGGAGCCTCTCTT  6360

Qy   6361 tgacctcttctagcatagaaatgcagcttctggtgaccggaaatgttaagggtaacattt  6420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6361 TGACCTCTTTCTAGCATAGAAATGGCAGCTTCTGGTGACCGGAAATGTTAAGGTAACATTTT  6420

Qy   6421 aatgatccattccatattctccacactgggaaggaaaattgtgattggtccattcaggcag  6480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6421 AATGATCCATTCATATTTTCCACACTGGGAAGGGAAAATTGTGATTGGTCCATTCAGGCAG  6480

Qy   6481 caggac  6486
          ||||||
Db   6481 CAGGAC  6486
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```
Qy   2461  ttatcactaaatgaatatgccagtcacggaggaggagacagatcttcttcttgtatgagtactcag  2520
           |||||| ||||||||| |||||||||||||||||||||||||| ||||||||||||||||||||||||
Db  25361  TTATACTAAATGAAATATGCCAGTCACGGAGGAGGAGACAGATTCTCTTCTTGTATGAGTACTCAG  25420

Qy   2521  agtggtctcattcaataaagtggaatggtagctgccaggggctcggaggggagctcgaggatgg    2580
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  25421  AGTGGTCTCATTCATAAAGTGGAATGGTAGCTGCCAGGGGCTCGGAGGGGAGTCGAGGATGG     25480

Qy   2581  gaagttaatgttagtaacaggtacggagagtccagttttgggaagataaaaagttctggagg     2640
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  25481  GAAGTTAATGTTAGTAACAGGTACGGAGAGTCCAGTTTTGGGAAGATAAAAAGTTCTGGAGG     25540

Qy   2641  tggatagtgccgacggttccacatgtcaatgcacttaatgccaccaaaactgtactcttaa    2700
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Db  25541  TGGATAGTGCCGACGGTTCCACATGTCAATGCACTTAATGCCACCAAAACTGTACTCTTAA     25600

Qy   2701  aaacagttgaccggcaccggtggtcacgcctg-aatcccagcactttgggagaccgagg     2759
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Db  25601  AAACAGTTGACCGGCACCGGTGGTCACGCCTGTAATCCCAGCACTTTGGGAGACCGAGG      25660

Qy   2760  cgggcgggatcacaaggtcaggagagatcagagacacatcctggctaacacggtgaaaccccgtc  2819
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Db  25661  CGGGCGGGATCACAAGGTCAGGAGATCGAGACCATCCTGGCTAACACGGTGAAACCCCGTC      25720

Qy   2820  tctactaaaaatacaaaaaaattagccgggcgtggtggcgggcgcctgtagtccagcta     2879
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Db  25721  TCTACTAAAAATACAAAAAAATTAGCCGGGCGTGGTGGCGGGCGCCTGTAGTCCAGCTA     25780

Qy   2880  ctcgggggggctgaggcaggagaagaatggctgaacctgggaggcggaggttgcagtgagctg  2939
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Db  25841  AGATCCAGCCACTGCACTCCAGCCTGGGCGACAAGAGCTAAGACTCCGTCTCAAACAAAACA    25900

Qy   3000  aagcaaaacaaaaacaaacagttaagatttttttttttttttttaaatgattcagtggaatag  3059
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Qy   3060  aatggattcttcaaatacttaacttagccacggggtgggataagggaaccctacttagtaagtatt  3119
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Qy   3120  tttccccttcttcttcttaaaaataagatcgaatcgatgtctaggttggaattaggcttcctgggc  3179
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Qy   3180  gacacatctaatgcaaagatcagcccacctcttttctgtaaggatctgatggtaaacatt     3239
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Qy   3240  tccaactt-gagagctatgtctcttgcagctactcagctctgctattgcagtgcaaaagcag  3298
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Qy   3299  ctaaaggcaacgtaaaggaatgacggaaggaggagccctttagttgttttattttacaaataagcttta  3358
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Qy   3359  tttgcaaaagcagatgcaaagccagacttagttgctgatctctgatctacagtcagaata     3418
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Qy   3419  cacagagaaggagagattttgccgtataattaattatctctcttgcaaaagcagtcc     3478
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Qy   3479  ataaaaaagtgaggacaaacctgggagaacacaaacatgtctgatgataga      3538
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Qy   3539  gcactaatattcttaattcaaaaaaagacatttttatcaaaagaagaagaaatacttagaaa  3598
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Qy   3599  attgtgcaaaagaccttccattttgttcataacgtaggaagaagcttgttttacttttcc  3658
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Db  26501  ATTGTGCAAAAAGACTTTCCATTTTGTTGCATAACGTAGGAAGAAGCTTGTTTTACTTTTCC   26560

Qy   3659  tatcatcttctaacttccagtaccagcctaattttgttattttattattatgttatta  3718
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Qy   3719  ttttggacaagagttcttgctctgtctcccaggctgggagtgcagtgacgatagctt  3778
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Db  26621  TTTTGGACAGAGTCTTGCTCTGTCTCCCAGGCTGGAGTGCAGTGGCGGGATAGCTT     26680

Qy   3779  acaacagctctacctcccaggttcaagaaatcttcccacttagctcccgagtagctg  3838
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Qy   3839  ggactgtaggcacatgccaccatggccagctaattttttttatttttttgtagagacagagtc  3898
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Db  26741  GGACTGTAGGCGCACATGCCACCATGGCCAGCTAATTTTTTGTATTTTTTAGTAGAGACAGAGTC   26800

Qy   3899  tcattatgttgccgaggctggtcttgaactcctcnagcagtctcctgcctcggc  3958
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Qy   3959  ctcccaaagtgttgggattacaggcgtaagctcccagcctattttgtatattt  4018
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Qy   4019  actataagttgttgaaggtcatgataagaactgccatattttttgtcgggaaatctatc  4078
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Qy   4079  accctcaagatcccaggagtccatggatatctgtttcttnagcagtcctcctggc  4138
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Qy   4139  ggcaatgcagagatggggagcccagagaatactccagcgttaacccaaggtgttgacagg  4198
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Qy   4199  tgggaaacagtggctacaatttgggagttcagtgggcgcagagaagggtgcaggg  4258
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Db  27101  TTGGAAACAGTGGCTAAATTTGGGGATTGCAGTGGGCACAAGGTGTTGACAGG      27160

Qy   4259  gtggccagaagggcccccagccacatcctagatggagccacaagtacagtgccaagggctcttg  4318
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Db  27161  GGGCCACGAAGGGCCCCAGCCACATCCTAGAATGGAGGCACAAGTACCAGTGCCAAGGCTCTTG   27220

Qy   4319  gtctgaattctgaaaacatttacctctgaccctggccacactggccatgctcgttgt  4378
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Db  27221  GTCTGGAATTCTGAAAACATTTACCTCTGACCCTGGCCAGCCCACTGGCCATTGCTTGTGT    27280

Qy   4379  gcagcccagttggcaggagaacctatccatgattgccgcctctcttttcggtccttcag  4438
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Db  27281  GCAGCCCAGTTGGCAGGGAAACCCTACCCATGATTGCCGCCTCTCTTTTCGGTCCTTCAG    27340

Qy   4439  tatgaaccagcatcacagtgcacttgtggcagatggcagtagccgggagctactc  4498
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Db  27341  TATGAACCCAGCCATCACAGTGCACTTGTGGCAGAAGTGGCATACCCGGGAGCTACTC   27400

Qy   4499  tcctccggccagatgccctttctcccccagtgccccgtccgtgtggcagctctaccccgggagg  4558
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Db  27401  TCCTCCGGCCAGATGCCCTTCTCCCCAGCTGCCCGTGCCCGCCTGGGCAGCTCTACCCCGGGAGG   27460

Qy   4559  aagtaccgagacgcggattccagtttctgggaaatagcagaacccatggccaggcaagtgtg  4618
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Qy   4619  tggtggttctaggtgaaagcagacagtggccctggactgcctggccctctcttc  4678
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Qy   4679  tgtgccctggccccctttggggtttctgtctcttgttgctcaagtcttctt              4738
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Db  27581  TGTGCCCCTGGCCCTTGGGGTTTCTGTCTCTTGTTGCTCAAGTCTTCCTT              27640

Qy   4739  caaggaggccctcagtcgtgtgtcggtgatggatcgagtcaggc                     4798
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Db  27641  CAAGGAGGCCCTCAGTGTGTGTCGGTGGCATGAGTCCCATGTGGGATGCAGGC           27700

Qy   4799  agagtggtgtgaggggagggaggggtttgcttccctgggc                        4858
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Db  27701  AGAGTGGGTGTGAGGGGAGGGGTTGCTTCCCTGGGCTAGGGAAATCCATAAGCTGGAGT      27760

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Qy   4919  caactggaagagcaatctccagaggttctcatgtgtgt                          4978
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Db  27821  CAACTGGAAGAGACAATCTCCAGAGGTTCTGATGGCTGTC                        27880

Qy   4979  tatggagcagctgttcctaacatatcagcc                                  5038
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Db  27881  TATGGAGCAGCTGTGGTCCTAACATATCAGCCCGGAC                           27940

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Db  27941  GGTATGTTGGGCGCCCTGTGCGTCTCCGTGT                                 28000

Qy   5099  ctctttcaagaaagaacgggcgtggcctcc                                  5158
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Qy   5159  atagccacctgtcacctcttgttcccccag                                  5218
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Qy   5219  ccccccataataagttcctaaagcatggga                                  5278
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Db  28121  CCCCCATAATAAGTTCCTAAAGCATGGGA                                   28180

Qy   5279  tgtgaggaatttgtagggtgtacgtgttaa                                  5338
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Db  28181  TGTGAGGAATTTGTGAGGTGTACGTGTTAAT                                 28240

Qy   5339  ctggggatggaatgaacttccctcgagaacc                                 5398
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Db  28241  CTGGGGATGGAATGAACTTCCCTCGAGAACCA                                28300

Qy   5399  atctcggtgtcctagatttaacca                                        5458
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Db  28301  ATCTCGGGTGTCCTAGATTTAACCATGGCACTG                               28360

Qy   5459  accagcaactgacccatagaaggg                                        5518
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Db  28361  ACCAGACAACTGACCCATAGAGAGGGCTCCTC                                28420

Qy   5519  caggccctggttccattggaggg                                         5578
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Db  28421  CAGGGCCTGGTTCCATTGGAGGGGCTGGCA                                  28480

Qy   5579  tggggtgccgggctccccccaatag                                       5638
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Db  28481  TGGGGTGCCGGGGCTCCCCCAATAGTTCAC                                  28540

Qy   5639  gctggccctgcctcttctggcctggt                                      5698
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Db  28541  GCTGGCCCCTGCCTCTTCTGGCTGGTGTC                                   28600

Qy   5699  tacctgcttcttctgtttgcacaccc                                      5758
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Db  28601  TACTTGCTCTTCTTGTTTCGTTTGCACACCC                                 28660

Qy   5759  cctgcaacactcagttcctctcgtttcctt                                  5818
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Db  28661  CCCTGCAACACTCAGTTTCTCTCGTTTTCCTT                                28720

Qy   5819  gtctgtacttaggggcagtcgcctgg                                      5878
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Db  28721  GTCTGTACTTAGGGCAGTCGCCTGGATGG                                   28780

Qy   5879  ccagttccccctgctggtcgcaagc                                       5938
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Db  28781  CCAGTTTCCCCTGCTGGTCGCAAGCTGTG                                   28840

Qy   5939  tcttctagatggcacactcccaaa                                        5998
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Db  28841  TCTTCTAGATGGCACACTCCCAAAATCCCT                                  28900

Qy   5999  ctccagcgacccccagtgcagctcc                                       6058
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Db  28901  CTCCAGCACCCCCAGTGCAGCTCCGTCGTG                                  28960

Qy   6059  tttaaagagatggcattagaggg                                         6118
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Db  28961  TTTAAAGAGATGGCATTAGAGGGAGCCCCAGTCT                              29020

Qy   6119  tcagttcctggtgacacttttggcccg                                     6178
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Db  29021  TCAGTTCTGTGGTGACACTTTGGCCCGGAAAATGA                             29080

Qy   6179  gagcctcagtgagcccatctgcacag                                      6238
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Db  29081  GAGCCCTCAGTGAGCCCATCTGCACACAGTGGGGA                             29140

Qy   6239  tctgcttattcagtcctt                                              6298
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Db  29141  TCTGCTTATTCAGTCCTTCAGCTCACG                                     29200

Qy   6299  gtactggttaattaaacttattgct                                       6358
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Db  29201  GTACTGGTTAATTAAACTTTATTGCTCACTG                                 29260

Qy   6359  tttgacctctttctagacataga                                         6418
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Db  29261  TTTTGACCTCTTTCTAGCATAGAAAATGGCAGC                               29320

Qy   6419  ttaatgatccattcattt                                              6478
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Qy   6479  agcaggac                                                        6486
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Db  29381  AGCAGGAC                                                        29388
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JOURNAL      Unpublished
REFERENCE    2  (bases 1 to 210791)
AUTHORS      Genoscope.
TITLE        Direct Submission
JOURNAL      Submitted (23-MAY-2001) Genoscope - Centre National de Sequencage :
             BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
             - Web : www.genoscope.cns.fr)
COMMENT      On May 30, 2001 this sequence version replaced gi:12657316.
             --------------------  Genome Center
             Center : Genoscope / Centre National de Sequencage
             Center code: GS
             Web site: http://www.genoscope.cns.fr/
             Contact: SeqRef@genoscope.cns.fr
             --------------------  Summary Statistics
             The following BAC sequence is oriented from the T7 to the SP6 end.
             Upstream BAC (overlapping the T7 end) : C-2588C21
             Downstream BAC (overlapping the SP6 end) : R-164H13 (AC=AL139020)
             --------------------
             Assembly program: Phrap; version 2.0
             Quality coverage: 7.83x in Q20 bases; sum-of-contigs
             --------------------
             Overall quality chart :
             --------------------
             Range       :  bases
             0    -   9  :
             1    -  19  :
             10   -  29  :          3
             20   -  39  :         34
             30   -  39  :         34
             40   -  49  :       1491
             50   -  59  :       5034
             50   -  59  :       7834
             70   -  79  :      22859
             80   -  89  :      63567
             90   -  99  :     109969
             --------------------
             Percentage of bases with a quality value >= 40 : 99 %.

FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /chromosome="14"
                     /clone="R-1070N10"
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                     RHdb:RH44553
                     dbSTS:STS37622
     STS             11476..11602
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                     RHdb:RH69831
                     /note="matching EMBL:R21904
     STS             34400..34562
                     dbSTS:STS49708
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                     RHdb:RH95830
                     /note="matching EMBL:Z16446
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                     RHdb:RH93740
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                     156248..156397
                     /note="matching EMBL:AA129468
                     RHdb:RH48023
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     STS             181393..181583
                     RHdb:RH45107
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                     RHdb:RH45537
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                     dbSTS:STS38605
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     STS             189248..189446
                     RHdb:RH7821
                     /note="matching EMBL:R70888
                     dbSTS:STS54563
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     STS             190708..190871
                     RHdb:RH98896
                     /note="matching EMBL:AA856757
                     dbSTS:STS68645
                     Identified using the e-PCR software (G. Schuler)"
BASE COUNT      55743 a    48482 c    5054 g    56512 t
ORIGIN
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Query Match            98.5%;  Score 6389.4;  DB 9;  Length 210791;
Best Local Similarity  99.6%;  Pred. No. 0;
Matches 6459; Conservative     0;  Mismatches    22;  Indels    7;  Gaps   5;

Qy      1 tcctcctcctccccctcctccccactggcacgcccccactgccggccccgcccccac      60
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Db 197489 TCCTCCTCCTCCCCCTCCTCCCCCGACTGGCCCGCCCCACTGCCGGCCCCGCCCCCAC 197548

Qy     61 tgccggcccgggccccaccccacgccggagctgctccatttaaggagagattgcgcaagtgga 120
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Db 197549 TGCCGGGCGCCCGGGCCCCACCCCACGCCGGAGCTGCTCCCAPTTAAGGAGATTGCCGCAGTGGA 197608

Qy    121 aagctacacgtgtgagcctagaggcgggtcccggtgttgcagaacttgccatgccctccgaag 180
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Db 197609 AAGCTACACGTGTGAGCCTAGAGGCGGGTCCCGGTTGCAGACTTGCCATGGCCTCCCAAG 197668

Qy    181 cttctgtgcgtctaggggtgccccctggccgtctgtggatccagagggcctggaatctacg 240
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Db 197669 CTTCTGTGCGTCTAGGGTGCCCCCTGGCCGTCTGTGGATCCAGAGGCCTGCGCATCTACG 197728

Qy    241 aagatgaggagaggagaaacctgggtgactgtgtcggttcaatccctcgcgtaggg 300
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Db 197729 AAGATGAGGAGAGGGAGAACCTGGGTGACTGTGTCGGTTCAATCCCTCGCGTAGGG 197788

Qy    301 aatgggccaggcgctcccaggcaagaagtgagtcctgggcacaggggaggcgtgtggg 360
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Qy    361 gagggctgcgcactgacccctgccgtgtgggaccgcaggtgggggtcagagggggccgtt 420
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Db 197849 GAGGGCTGCGCGCACTGACCCCTGCCCGTGTGGGACCGCAGGTGGGGGTCAGAGGGGGCCGTT 197908

Qy    421 ctcaccccgcactggaaaactcacttctgtcgaaggtctaggagggcagcaaatgtccatgcc 480
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Db 197909 CTCACCCCGCACTGGAAAAACTCACTTCTGTCGCAGGTCTAGGAGGGCAGCAAATGTCCATGCC 197968

Qy    481 cagcctggcccccaggaacacccccgtaaaggggaccacacaggcacacaagcttatccacatg 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 197969 CAGCCCTGGCCCCCAGGAACACCCCCGTAAAGGGACCACACAGGCACACAAGCTTATCCACATG 198028
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Qy   541 agataactgtggtccctgcgttggtgaagccgaggccaggctcaaggtcaggcttagtgccatt 600
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Db 198029 AGATAATGTGGGTCCTCGCGTGCGTGGTCAGAAGCCGAGGTTAAGGTAGTTCAGGGCTTAGTGCCATT 198088

Qy   601 cccagtgcctgctggggaaggccaacacaaatggggcagcagctattgagctgggcttgtgggat 660
         |||| ||||||||||||| |||||||| ||||||||||||||||||||| ||| |||||| |||||
Db 198089 CCCAGTGCCTGCTGCTGGGAAGGCCCACAAATGGGGCAGCAGCTATTGAGCTGGGCTTGTGGGAT 198148

Qy   661 gagtaggagagttcctccagggtcctagaaagaggaggcaaggagtagtataacaaagcattgcag 720
         ||||||||||||||||||||||| |||| |||||||||||||||| || |||||||| |||||||||
Db 198149 GAGTAGGAGAGTTCCTCCAGGGTTCTAGAAAGAGGAGGCAAGGAGCTAGTATAACAAAGCATTGCAG 198208

Qy   721 cctggaggcaccaggtgggccaacaggagtgaacatgacattggtgtcagattaccttgatct 780
         ||||||||||||||||||||| ||||||| || ||||||||||||||| | |||||||| |||||
Db 198209 CCTGGAGGCACCAGGTGGGCCAACAGGAGTGAACAGATGACATTGGTGTCAGATTACTTGATCT 198268

Qy   781 gcaaaatgagaatatatacccttcttgtggcaagctagtcacaacatgctacacatgg 840
         || |||||||| || |||||| |||| ||||||||||| || ||||||| || | |||||
Db 198269 GCAAAATGAGAATAATATACCTTCTTGTGGCAAGCTAGTCACACAGACATCTCACATACATGG 198328

Qy   841 ctcaccgcctgaatgcctggggaagcatttgactgataaacagatcctcgaaaattaattc 900
         ||||||||||||| ||||||||||| ||||||||||| |||||| |||| ||||||||||||
Db 198329 CTCACCGCCTGAATGCCTGGGGAAGCATTTGACTGATAAACAGATTCTGAGAAAATTAATTC 198388

Qy   901 aggaggcttgggtgagtcctagattcttaactttcaaaagcctcccaggtgtgataatgac 960
         |||||| |||||||||| |||||||||||||||||| |||||| |||| |||||||| ||||
Db 198389 AGGAGGCTTGGGTGGGAGTCCTAGATTCTTTACTTTCAAAAGCTCCCCAGGTGTGATAATGAC 198448

Qy   961 taatgacttcaggaaacggctgtagatcgagatgagggcttagtcacagccagtctttgaggat 1020
         ||||||| |||||||||| ||| ||| ||||||||||||||||||| || ||||||||||| |||
Db 198449 TAATGACTTCAGGAAACGGCTGTAGATCGAGATGAGGGCTTAGTCACAGCCAGTCTTTGAGGGAT 198508

Qy  1021 gaagtaaataacagtagcgtctctgtgtggttggggaattgattccaggaccga 1080
         ||||||| |||| || ||||| |||||||||||||||||||||||||||||||||
Db 198509 GAAGTAAATAACAGTAGCGTTTCTGTGTGGGTGGGGAATTGATTCCAGGACCGA 198568

Qy  1081 ctgtggatgctcaagtccctgatagagaaatgacctgggtagtaattacatattaaccctcag 1140
         ||||||||||||||||| ||||| ||||||||||||||||| ||| ||||||||||||||||||
Db 198569 CTGTGGATGCTCAAGTCCCTGATAGAGAAATGACCTGGGTAGTAATTACATATTAACCCTCAG 198628

Qy  1141 cgcatcctctactatattgaaatcagatttcctaataacctaatgctacaactacaca 1200
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Db 198629 CGCATCCTCTACTATATTTGAAATCAGATTTCCTAATAACCTAATGCTACAACTACACA 198688

Qy  1201 tcacttcaagctctgctttgggaaatttcttttttttccccaaatatttt 1260
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Db 198689 TCACTTCAAGCTCTGCTTTGGGAAATTTCTTTTTTTTCCCCAAATATTTT 198748

Qy  1261 aatctgaggttagtcgaattcatgggtgcagtaccatggaaatgggggggctggctgac 1320
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Db 198749 AATCTGAGGTTAGTCGAATTCATGGGTGCAGTACCATGGAAATGGGGGGGCTGGCTGTAC 198808

Qy  1321 cttagttgtatgtgttcagtatccggatatttaaaatgccattaggggctgggcggc 1380
         || ||| |||||||||||||| ||||||||||| ||||||||||||||||||||||||
Db 198809 CTTAGTTGTAATGTGGTTAAAAGCATATCCGGATATTTAAAATGCCATTAGGGGCTGGGCGGC 198868

Qy  1381 ggtggctcacgcctgtaatcccagcacttgggagccagatgggcttatcacggagatc 1440
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Db 198869 GGTGGCTCACGCCTGTAATCCCAGCACTTGGGAGGCCGAGATGGGCTTATCACGGAGATC 198928

Qy  1441 aggagatcgagacatcctagccacacatgggaaacccagtctctactaaaaatacaaa 1500
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Qy  1501 aattagccggggccgttggtcggcgacgcctgtagtcccagctactcgggaggctgaggcagg 1560
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Qy  1561 agaatggcgtgaacccggagcgaagcttgtagtgagccgagatcgcacccactgcactc 1620
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Db 199049 AGAATGGCGTGAACCCGGGAGGCGGAGCTTGTAGTGAGCCGAGAATCGCACCACTGCACTC 199108
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Qy  1621 cagcctgggtgacagagtgagactccgtcccaaaaaaaaaaaaaaaaatgccgtt 1680
         ||||||||||||| ||| ||||||||||||||                      
Db 199109 CAGCCTGGGTGACAGAGTGAGAGTGAGACTCCGTCC---AAAAAAAAAAAAAAAAATGCCGTTT 199165

Qy  1681 aggtctctgaaaccaattccactgcctgtttgtttgtttgtttttttacagtt 1740
         ||| |||||| ||||| || |||||||||||||||||||||||||||||||||||
Db 199166 AGGTCTTCGTAAACAATTCACTGCCTGTTTGTTTGTTTGTTTTTTTGAGAAAGTCTTGCTCTGTT 199225

Qy  1741 gcggctggagtgcactgttgtgatgttggctcactgcaacctccacctcccaggttcaag 1800
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Qy  1801 tgattctcatgcctcaagcctccgggagttagcttggattacaggtgcatgc 1860
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Db 199286 TGATTCTCATGCCTCAGCCTCCCGAGTAGCTGGGATTACAGGCGATTACAGGTT 199345

Qy  1861 aattttttttgtttattttccaggagagacaaaagtttaatcatgtgggccaggctggtttt 1920
         ||||| ||||| |||||||||||| |   ||||||||||||||||||||||||||||||||||
Db 199346 AATTTTTTTTGTTTATTTTCCAGGAGAC-AAAGTTTAATCATGTGGGCCAGGCTGGTTTTT 199404

Qy  1921 gaactcctgacctcaagtgatctgcccacctggcctcccaaagtgctggat 1980
         |||||||||| ||| ||||| |||||||||||||||| |||||||||||||||
Db 199405 GAACTCCTGACCTCAAGTGATCTGCCCACCTTGGCCTCCCAAAGTGCTGGAT 199464

Qy  1981 gagccacctcgtcccagccagttcactgacactttaaacaataacacattcctaaaa 2040
         |||||||||||||||||||||||||||||||||||||||||||| ||||| ||||||||
Db 199465 GAGCCACCTCGTCCCAGCCAGTTCACTGACACTTTAAACAATATAAACACATTTCCTAAAAA 199524

Qy  2041 aagttcaaataggttatttcaaaaaaatgttggttgtaggagaacatgggaaaagtcttctgtac 2100
         ||||||||||||||||||||||||||| |||| |||||||||||||||||||||||||||| ||||
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Qy  2101 atacactaaataaagcatgcaaaaattgtgggagcaaatatttaagttttttcaaaagcct 2160
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Db 199585 ATACACTAAATAAAGCATGCAAAAATTGTGGGAGCAAATATTTTAAGTTTTTCAAAAGCCT 199644

Qy  2161 gaaaaagtgttaatggagggcacttgtaaatggtgcagccacacttgggaaacaaggatgag 2220
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Db 199645 GAAAAAGTGTTAATGGAGGGCACTTGTAAATGGTGCAGCCACACTTGGGAAACAGGATGAG 199704

Qy  2221 gattctcaaaaagaagaattacgggcatatccagcaatgccacttctggattatatcccca 2280
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Db 199705 GATTTCTCAAAGAAGAAATTACGGGCATAATCCAGCAATGCCGCGTTCTGGATATATACCCA 199764

Qy  2281 caagactctggaagccggaacttaagcatgtgattccatacatccatgttcacagcagtatca 2340
         || |||||||||||||||||||||||||| |||||| |||||||||||||||||||||||||||
Db 199765 CAAGACTCTGAAGCCGGAACTTAAGCATGTATTCATCACATCCATGTTCACAGCAGTATCA 199824

Qy  2341 tccatactagccaaaaggttagctgtccccgtgtccattgataggaatggggtaaac 2400
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Db 199825 TTCATACTAGCCAAAAGGTTGGGCAGCCCCAGTGTCCATTGATAGAATGGGGGTAAC 199884

Qy  2401 aacacaaaccatgaagttattccacccttaaaagtcagacaacacggatgaaacttggagcca 2460
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Db 199885 AACACAAACCATGAAGTTATTCACCCTTAAAAGTCAGACAACACGGATGAAACTTGGAGCCA 199944

Qy  2461 ttatactaaatgaaaatatgccactcacaggaaggacagaatctcttttgatgtgagtag 2520
         ||| ||||| |||||||| ||||||||||||||| |||||| || |||||||||||||||||
Db 199945 TTATACTAAATGAAATATGCCACTCACAGGAAGGACAGATTCTCTTGTGTTGATGAGGTACTCAG 200004

Qy  2521 agtggtctcattcataaagtcggaatggtagctgccaggggtctgagggagtcgagagtgg 2580
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Qy  2581 gaagtttaaatgttagtaacagtacggagtctcagtttgggagaataaaaagttctggagg 2640
         |||| ||||||| |||||||||||||||||||| |||||| |||||||||||||||||||||
Db 200065 GAAGTTTAAATGTTAGTAACAGTACGGAGTCTCAGTTTGGGAAGAATAAAAAAGTTCTGGAGG 200124

Qy  2641 tggatagtgccgacggttccaccatgtcaatgcacttaatgccaccaaactgtactcttaa 2700
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Db 200125 TGGATAGTGCCGACGGTTCCACCATGTCAATGCACTTAATGCCACCAAACTGTACTCTTAA 200184

Qy  2701 aaacagttgaccgggcacggtggctcacgccctg-aatcccagcacttggggaccgagg 2759
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Db  200185 AAACAGTTGGCCGGGTGCCGGTGCGTGGCTCACGCCTGTAATCCCAGCGACTTTGGGGGCCGAGG                        200244
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Qy    2760 cgggccggatcacaagtcaggaggagatcgagaccatcctggctaacacggtgaaaccccgtc                            2819
Db  200245 CGGGCGGATCACAAGGTCAGGAGGATCAGAGACCATCCTGGCTAACACGGTGAAACCCCGTC                              200304
Qy    2820 tctactaaaaatacaaaaagaattagccgggtgcgggtggtcttgtagtcccagcta                                  2879
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Qy    2880 ctcggggggggctgaggcaggagaatggcttgaacctgggaggcggaggttgcagtgagctg                             2939
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Db  200365 CTCGGGGGGGCTGAGGCAGGAGAATGGCTTGAACCTGGGAGGCGGAGGTTGCAGTGAGCTG                               200424
Qy    2940 agatccagccactgactccagcctgggcgacagagagcaagactccgtctcaaacaaaaca                              2999
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Db  200425 AGATCCAGCCACTCGACTCCAGCCTGGGCGACAGAGCAAGACTCCGTCTCAAACAAAAACA                               200484
Qy    3000 aagcaaaacaaaaacaagttaaagatttttttttttaaatgtaaatggaaatag                                     3059
           ||||||||||||||||||||||||||||||||||||||||||||||
Db  200485 AAGCAAAACAAAAACAAGTTAAAGATTTTTTTTTTTTTTTTAAATGATCAGTGGAAATAG                                200544
Qy    3060 aatggattcttcaaatacttagccacgaggtgggataaaggagacctacttaagtaatt                               3119
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Qy    3120 tttccccttctttttatataaaatagatcatgatgttttaggtgcttcctgggc                                      3179
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Db  200605 TTTCCCCTTCTTTTCTTAAAAATAGATCGATGTCTTAGGGTGGGAANTAGGGC                                       200664
Qy    3180 gacacatctaatgcaaagatcagccacaccttttctgtaaaagatctgatggtaaacatt                               3239
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Db  200665 GACACATCTAATGCAAAGATCAGCCACCTTTTCTGTAAAGGATCTGATGGTAAACATTT                                 200724
Qy    3240 tccactt-gagagctatagctcttgcagctactcagtcctgctattgcagtgcaaaagcag                              3298
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Db  200725 TTTGCAAAAGCAGATGCAAAGGCTATGCTCTTGCAGCTACTCAGTCTCTGCTATTGCACAGTCACGAANTA                     200784
Qy    3299 ctaaagcaacgtaaaggaatgacggaagagagccttagttatttattttacaataaaagttta                            3358
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Qy    3359 tttgcaaaagcaagtgcaagccagacacttagttgttttgctgatctctgatctacagtcaggaata                         3418
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Qy    3419 cacagagaaggagagagattttgccgtataattttaaaatacttctctttttgcaaaagcagtcc                           3478
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Qy    3479 ataaaaaagtgaggcacacaaactgagaaaaattattccacacaatgtctgattgataga                               3538
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Db  200965 ATAAAAAAAGTGAGGACGAGAGAATTTGCCGTANTAANTTTAAAANTACTTCTGATTGATAGA                              201024
Qy    3539 gcactaatattcttaattcaaaaagacatttatcaccaaaagaacaaatacttagaaa                                 3598
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Qy    3599 attgtgcaaaagacatttcccatttgttgcataacgtaggaagactttggtttttacttttcc                             3658
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Qy    3659 tatcatcttcttaacttccagtaccagcctaatttgtattttgttattttattttatgtattta                            3718
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Qy    3719 ttttgagacagagtcttgctctctcccaggctggagtgcagtgacgcagatagctt                                    3778
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Qy    3779 acaacagcctctacctcccaggttcaagaaatcttcaccttagcttcccgagtagctg                                 3838
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Db  200185 ... (continued)
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Db  201265 ACAACAGCGCTTCTACCTCCCAGGTTCAAGAAACTCTTCTCACCTTAGCTTCCCGAGTAGCTG                              201324
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Qy    3839 ggactgtaggcacatgccacacatggccagcttaattttttatttttgtagagacagagtc                              3898
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Qy    3899 tcattatgttgtcgcgaggctggtcttgaactcgtggacctgacctcctgcctggc                                    3958
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Qy    3959 ctcccaaaagtgtttgggattacaggcataagcacactgctcccagccctatttcgtatatt                             4018
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Qy    4019 actataaagttgtgtcgaaggtcatgatcagaaagctctttaaaacgaagatttaaaaaattac                            4078
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Qy    4199 ttggaacagtggctaaatttgggattgcagtgtgtggggtcgaggtgcagggtcaggag                                 4258
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Qy    4259 gggccagaagggccccagccatcctagatgagcacaagtaccagtgccaaggctctg                                   4318
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Qy    4379 gcagccacagttggcagggaacccctatccatgactgtggccgccttttctggtccttcag                               4438
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Qy    4439 tatgaacccagcaatacaagtgcacttgtgtggcgagtgcatcaacagaggggagctactc                               4498
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Qy    4499 tcctccgggccagatgccctctccagctgccccgcctgtggcagctctaccccgggagg                                 4558
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Db  201985 TCCTCCGGGCCAGATGCCCTTCTCCCAGCTGCCCCGCCTGTGGCAGCTCTACCCGGGACTACTC                             202043
Qy    4559 aagtaccgagcacgcggattccagttcctggaaatagcagaccatggccaaggtgtg                                   4618
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Qy    4619 tggtggttctaggtgaadcgacagttgggccctcgttcactgccctctctcctc                                      4678
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Qy    4679 tgtgcccctggcccctcctgggtgtttctgttgtctcctctgtctgcttcaagtcttcctt                               4738
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Qy    4739 caaggaggcctcgagtgtgtcggtcggatcggtgcatcgagttcccatgtgggatgcaggc                               4798
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Qy    4799 agagtggggtggaggagggaggatttgcctcccctgggcttgctaggggaaatccataagctggagt                         4858
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Qy    4859 tccaactgcctcaccctgcctgctgctgccagcttagggccagcctgcattgggcggccgttaagc                          4918
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Qy    4919 caactggaagagacatcccagagaggtttcatggctggctgtcctctcctgccagattgactc 4978
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Db  202404 CAACTGGAAGAGACCATCTCCCAGAGGTTCTGATGGCTGTGCTCCTCTCCCTGCCAGATTGACTC 202463

Qy    4979 tatggagacagctggtcctaacatatcagccggagaggaaagactgacactggagtcggct 5038
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Qy    5039 ggtatgttggggccctggcgctctcggtgtagggatcagacgaaagtgagagaaacctctc 5098
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Qy    5099 ctctttctcagaaagaggggcccgtggcctcctcctctctgtcctgtggagattttcttac 5158
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Qy    5159 atagccacctgtcaacctctgttccccagacccctggatgtgtgtacacagtgggtggg 5218
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Qy    5219 ccccccataataagttcctaaaagcatgggatctccatcgaataagactcatttaatcct 5278
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Qy    5459 accagcacactgaccctagagggctcccctccaggatgggcacagcagctggagcaggccagg 5518
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Qy    6359 tttgacctcttctagcatagaaatggcagctctgtacggaaatgttaaggtaacatt 6418
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RESULT 4
AB025272S3

LOCUS   AB025272S3   1717 bp   DNA   PRI   14-APR-2000
DEFINITION Homo sapiens TML1 gene for TCL1 / MTCP1-like 1, exon 3 and complete
            cds.
ACCESSION   AB025274
VERSION   AB025274.1 GI:5478618
KEYWORDS   TML1; TCL1 / MTCP1-like 1.
SEGMENT   3 of 3
SOURCE   Homo sapiens DNA, clone:pCOS231.
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (sites)
  AUTHORS   Sugimoto,J., Hatakeyama,T., Narducci,M.G., Russo,G. and Isobe,M.
  TITLE   Identification of the TCL1/MTCP1-like 1 (TML1) gene from the region
            next to the TCL1 locus
  JOURNAL   Cancer Res. 59 (10), 2313-2317 (1999)
  MEDLINE   99274532
REFERENCE   2 (bases 1 to 1717)
  AUTHORS   Isobe,M., Sugimoto,J. and Hatakeyama,T.
  TITLE   Direct Submission
  JOURNAL   Submitted (24-MAR-1999) to the DDBJ/EMBL/GenBank databases.
            Masaharu Isobe, Toyama University, Faculty of Engineering; Gofuku
            3160, Toyama, Toyama 930-8555, Japan
            (E-mail:isobe@eng.toyama-u.ac.jp, Tel:+81-76-445-6872,
            Fax:+81-76-445-6874,
FEATURES   Location/Qualifiers
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Db   61 TCGGTGCATGAGTTCCCATGTGGGGATGCAGCAGAGTGGGGTGAGGGGAGGGGTTGCCT 120

Qy 4827 tccctgggctaggggaattcatataagctggaagtcccacccctgcctcactgtc 4886
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Db  121 TCCCTGGGCTAGGGAAATTCCATATAAGCTGGAGTTCCCACCCCTGCCTCGCTGTC 180

Qy 4887 tgctgccagcctgcatggggcgcgttaagcgacactggaagacattcccagaggttc 4946
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Qy 4947 tgaatggctgctccctcctcctgcaagttgactcatatggagcagctggtcctaacatatcag 5006
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Db  241 TGATGGCTGCTCCCTCCTCCTGCAAGTTGACTCATATGGAGCAGCTGGTCCTAACATATCAG 300

Qy 5007 ccggagaggaaagactgacactgggaagtggcctggctatgtgttggggcccctgtgtctcggt 5066
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Db  301 CCGGAGAGGAAAGACTGACACTGGGAGGTGGCTGGTATGTGTTGGGGCCCCTGTGTCGGT 360

Qy 5067 gtaggaatcagacgaaagtgagagagacctctcctccctcctttcagaaagacgggcggtggcctcc 5126
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Db  541 ATCTCATCGAATAAGACTCATCATTTAATCCTTGTGAGGAATTTTGTGAGGTGTACGTGTTT 600

Qy 5307 aatgtcccatttcacgacagaaaaacaagaactcctgggggatgggaataacttcctcgagac 5366
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Db  601 AATGTCCCATTTCACGACAGAAAAACAAGAACTCTGGGGATGGGAATGGACTTCCTCGAGAC 660

Qy 5367 catacagccaggaaatagcggtgaatctgaatctctcgggtccctagatttaaccatggc 5426
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Db  661 CATACAGCCAGGAAATAGCGGTGAATCTTAGTGAATTCGGGTCCCTAGATTTAACCATGGC 720

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Db  721 ACTGAAGGTGCCGTGTGACGGTGGCCTTGGAGGGACCCAGCACTGACCCTAGAGGGCTCCT 780

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Qy 5667 ctcctcatgccccctcagtgaggaatcttcaatgtaacctgctcctctttctgtttgcacaccagc 5726
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Qy 5727 atagcctccttgcaggggcaggagaaggttaggggcccctgccacactccagtttctcctcgttttc 5786
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AUTHORS   Sugimoto,J., Hatakeyama,T., Narducci,M.G., Russo,G. and Isobe,M.
TITLE     Identification of the TCL1 locus
          next to the TCL1/MTCP1-like 1 (TML1) gene from the region
JOURNAL   Cancer Res. 59 (10), 2313-2317 (1999)
MEDLINE   99274532
REFERENCE 2  (bases 1 to 1722)
AUTHORS   Isobe,M., Sugimoto,J. and Hatakeyama,T.
TITLE     Direct Submission
JOURNAL   Submitted (12-OCT-1998) to the DDBJ/EMBL/GenBank databases.
          Masaharu Isobe, Toyama University, Faculty of Engineering; Gofuku
          3160, Toyama, Toyama 930-8555, Japan
          (E-mail:isobe@eng.toyama-u.ac.jp, Tel:+81-76-445-6872,
          Fax:+81-76-445-6874)
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Db   601 CAGTGGGTGGCGGCCCCCATAAATAAGTTCCTAAAGCATGGGAGATCTCATCGAATAAGACTCAT 660

Qy  5268 catttaatcccttgtgagaattcttgtgaggtgtagcgtgttaatgtcccatttcacgacgaa 5327
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Db   661 CATTTAATCCCTTGTGAGAATTTTGTGAGGTGTACGTGTTAATGTCCCATTTCACGACGAA 720

Qy  5328 aagacaagagactctgggggatggggaatgaactgact cctctgagaccaatacagccaagtaagcgg 5387
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Db   721 AAGACAAGAGACTCTGGGGATGGGGAATGAACTTCCTCGAGACAATACAGCCAAGTAAGCGG 780

Qy  5388 tgaaatctagtgatctcgggtccctagaattcaccatgggcactgaggtgccgtgacggt 5447
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Db   781 TGAAATCTAGTGATCTCGGGTCCCTAGAATTTAACCATGGCACTGAGGTGCCGTGACGGT 840

Qy  5448 ggcctggaggaacccagcaactagaggaggctcctctcagatgggcagcagcttgg 5507
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Db   841 GGCCTTGGAGGACCCCAGCAACTGACCCATAGAGGGCTCCTTCACAGATGGGCAGCAGCTTGG 900

Qy  5508 agcaggccaggcaggggcctggtcctggtcattggaagggggctggcaactggacttgaccc 5567
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Db   901 AGCAGG-CAGGCAGGGGCCTGGTCCATTGGAGGGGGCTGGCACTGGACTTGCCTTTGACCCC 959

Qy  5568 agcagcttgatgggggtgccgggggtcccccccatagttcaactgactgtctcctttggtcttc 5627
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Db   960 -AGCAGCTTGGATGGGGGCTGCGGGGGTCCCCCCATAGTTCAACTGACTGTCTCCTTTGGTCTTC 1019

Qy  5628 tcggcaggaccctgctgctggccctgccctcttctttgggctggtcgttctccaatgcccaagtga 5687
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Qy  5688 ggatcttcattgtacctgctctcttcttgtttgcaccaccagcatagcctccttgcaggcagaa 5747
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Db  1080 GGATCTTCATGTACCTGCTCTCTTCTTGTTTGCACACCACCAGCATAGCCT-CTTGCAGGCAGAA 1138

Qy  5748 ggcagtaggggcccctgcacacatcagtttctctctgtttcttccttagttatcaagtcctcct 5807
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Db  1139 GGCAGTAGGGCCCCTGCACACTCAGTTTCTCTCTGTTTCCTTAGTTATCAGTCCTGTCCT 1198

Qy  5808 gtcccacctcaggtctgtacttagggcagctgcctggaggtgggcttcaactgggggccctgtc 5867
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Db  1199 GTCCCACTCAGGTCTGTACTTAGGGCAGCTGGCCTGGATGGGCTTCAACTGGGGCCCTGTC 1258

Qy  5928 cctcaatgctgatcttcctagatgccacctcccaaatcccccttcatcaccacaggatgtgtg 5987
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Db  1319 CCTCAATGCTGATCTTCTAGATGCCACTCCCAAATCCCCTTCATCACCACCACAGGATGTGTG 1378

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Db  1379 CCCAGACCAAGGCCTCCAGCACCCCAGTGCAGCCTCGTGATTGGAAACTCACCATCGGCCAGG 1438

Qy  6048 cagtggttccgttttaagacgagggagcccagtctcggatgtggacttggatg 6107
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Qy  6108 ccctgtgggtgtattcagttctgctgacacttggccgaaatagatccagtgctgagcaagc 6167
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Qy  6168 aaagtacaccggagcctcagtgagccaatctgacacagtggaggagcatggaggatgggtt 6227
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Qy  6228 tggcctgtgcttctgcttattcagtcctccagctcacgagaggaagtgctagtccgtgaag 6287
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Db  1619 TGGCCTGTGCTTCTGCTTATTCAGTCCTTCAGCTCACTCACGGAAGGGAGTGCTAGTCCGTGAAG 1678

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RESULT        6
AF110466
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LOCUS       AF110466    1152 bp    mRNA             PRI    18-MAR-1999
DEFINITION  Homo sapiens T-cell leukemia/lymphoma 1B (TCL1B) mRNA, complete
            cds.
ACCESSION   AF110466
VERSION     AF110466.1  GI:4324704
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1152)
  AUTHORS   Pekarsky,Y., Hallas,C., Isobe,M., Russo,G. and Croce,C.M.
  TITLE     Abnormalities at 14q32.1 in T cell malignancies involve two
            oncogenes
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 96 (6), 2949-2951 (1999)
  MEDLINE   99178995
REFERENCE   2  (bases 1 to 1152)
  AUTHORS   Pekarsky,Y., Hallas,C. and Croce,C.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-DEC-1998) KCI, Thomas Jefferson University, 233 South
            10th Str. BLSB 1032, Philadelphia, PA 19107, USA
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BASE COUNT      232 a    325 c    324 g    271 t
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Query Match             10.8%;  Score 701.2; DB 9;  Length 1152;
Best Local Similarity   99.6%;  Pred. No. 8.9e-159;
Matches  703; Conservative   0; Mismatches   3; Indels   0; Gaps   0;
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Qy    5628 tcgcaggccctgctggccctctctggcctggtgtctcctcatgcccctcagtga 5687
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Db     424 TGGCTGGCCCTGCTCTGGCCCTCTTCTCGGCCTTCGTGTGTCTCCTCCATGCCCCTCAGTGA 483

Qy    5688 ggatcttcatgtacctgctctctgtttgcacacaccagcagcaatagcctcctt gcaggcagaa 5747
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Db     484 GGATCTTCATGTACCTGCTCTCTGTTTGCACACACCATAGCCTCCTTGCAGGCAGAA 543

Qy    5748 ggcagtagggccctcgcacactcagtttctctctgtgttctccttagttatcagtcctgtcct 5807
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Db     544 GGCAGTAGGGCCCTCGCACACTCAGTTTCTCTCTGTGTTTCCTTAGTTATCAGTCCTGTCCT 603

Qy    5808 gtcccactcaggtctgtaacttaggggaagtcggcctggacttggggcctgtc 5867
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Db     604 GTCCCACTCAGGTCTGTACTTACGGGGAAGTCGGCCTGGACTTGGGGCCTTGTC 663

Qy    5868 tgtgtgctgagccagttccccctgctggctcgcaagctgtgggtttcttcttctccctgtgcc 5927
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Db     664 TGTGTGCTGAGCCAGTTTCCCCTGCTGGCTCGCAAGCTGTGGGTTTCTTCTTCTCCCTGTGCC 723

Qy    5928 cctcatgctgatctctctagatgccactcccaatccccttcataccccaccagagatgtgtg 5987
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Db     724 CCTCATGCTGATCTCTCTAGATGCCACTCCCAAATCCCCTTCATACCCCACCAGAGTGTGTG 783

Qy    5988 cccagcaggcctccagcacccccacgtgcagctcgttggtgggaaactcaacatcggcgagg 6047
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Db     784 CCCAGCCAGGGCCTCCAGCACCCCCAGTGCAGCTCGTCGTGATTGGAAAACTCACCATCGGCAGG 843
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RESULT   7
LOCUS       AB035343    3144 bp    mRNA             PRI    12-DEC-2000
DEFINITION  Homo sapiens TCL6f4 mRNA for T-cell leukemia/lymphoma 6 ORF105,
            T-cell leukemia/lymphoma 6 ORF72, complete cds, clone:pDG4.
ACCESSION   AB035343
VERSION     AB035343.1  GI:8176590
KEYWORDS    T-cell leukemia/lymphoma 6 ORF72; TCL6f4; T-cell leukemia/lymphoma
            6 ORF105.
SOURCE      Homo sapiens cell line:Daudi cDNA to mRNA, clone:pDG4.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3144)
  AUTHORS   Saitou,M., Sugimoto,J., Hatakeyama,T., Russo,G. and Isobe,M.
  TITLE     Identification of the TCL6 genes within the breakpoint cluster
            region on chromosome 14q32 in T-cell leukemia
  JOURNAL   Oncogene 19 (23), 2796-2802 (2000)
  MEDLINE   20309940
REFERENCE   2  (bases 1 to 3144)
  AUTHORS   Isobe,M., Saitou,M. and Sugimoto,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-NOV-1999) to the DDBJ/EMBL/GenBank databases.
            Masaharu Isobe, Toyama University, Materials and Biosystem
            Engineering, Faculty of Engineering; 3190 Gofuku, Toyama 930-8555,
            Japan (E-mail:isobe@eng.toyama-u.ac.jp., Tel:+81-76-445-6874,
            Fax:+81-76-445-6872,
FEATURES             Location/Qualifiers
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                     /db_xref="GI:8176591"
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Db     844 CAGTGGTTCGGTTTAAGAGATGGCATTAAGAGGGAGCCCAGTCTGGATGTGGACTTGGATG 903

Qy    6108 ccctgtgggttatcagttctgtgacacttggcccggaaatagatccagtgctgagcaagc 6167
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Db     904 CCCTGTGGGTATCAGTTCTGTGACACTTGGCCCGAAATAGATCCAGTGCTGAGCAAGC 963

Qy    6168 aatgtacacacggagcctcagtgagcccatctgcacacttggccgaaatagaatccagtgctt 6227
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Qy    6228 tggcctgtgttctgttattcagtcctteaagtcacggaagggatgctagtccgtgaag 6287
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Db    1024 TGGCCTGTGTTCTGCTTATTCAGTCCTTCAAGTCACGGAAGGGATGCTAGTCCGTGAAG 1083

Qy    6288 gtgacctcacagtactggttaattaaacttattgtcactgtcca 6333
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Db    1084 GTGACCTCACAGTACTGGTTAATTAAACTTTATTGCTCACTGTCAA 1129
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BASE COUNT   764 a   809 c   809 g   762 t
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Best Local Similarity   10.8%;   Score 701.2; DB 9; Length 3144;
Matches 703; Conservative   0; Mismatches   3; Indels   0; Gaps   0;

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Db  2416  TGGCTGGCCCTGCTGGCCCTGGCCTCTTCTGTTGTCCTCCATGCCCCTCAGTGA  2475

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Db  2476  GGATCTTCATGTACCTGCTCTCTTCTGTTTGCACACCAGCATAGCCTCCTTGCAGGCAGAA  2535

Qy  5748  ggcagtaggcgccctgcacactcagttttctctcgtttctcttagttatcagtcctgtcct  5807
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Db  2536  GGCAGTAGGCGCCCTGCACACTCAGTTTTCTCTCGTTTCTCTTAGTTATCAGTCCTGTCCT  2595

Qy  5808  gtcccactcaggttctgtacttagggcaagctggcctgatgggggcctcactgggggcctc  5867
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Db  2596  GTCCCACTCAGGTCTGTACTTAGGGCAGCTGGCCTGGATGGGGCTTCACTCGGGGCCCTGTC  2655

Qy  5868  tgtgtgtctgagccaagttcccctgtcgtgctgcaagctgtggttgtctttctctctgtgcc  5927
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Db  2656  TGTGTGCTGAGCCAGTTTCCCCTGCCTGGCTGCAAGCTGTGGTTCTTTCTCTCCTGTGGCC  2715

Qy  5928  cctcatgctgatcttctagatgccactccaaatcccctccaccaccaggatgtgtg  5987
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Db  2776  CCCAGCCAGGCCTCCAGCACCCCCAGTGCAGTCGTCGTGATTGGAAACTCACCATCGGCAGG  2835

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Db  2956  AATGTACACACGGAGCCCTCAGTGAGCCCCATCTGCACAGTGGGGAGCAATGAGGGAGATGGGTT  3015

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Qy  6288  gtgacctcacaagtactgttattaaacttattgctctcactgtca  6333
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REFERENCE   1 (bases 1 to 3240)
AUTHORS   Saitou,M., Sugimoto,J., Hatakeyama,T., Russo,G. and Isobe,M.
TITLE   Identification of the TCL6 genes within the breakpoint cluster
            region on chromosome 14q32 in T-cell leukemia
JOURNAL   Oncogene 19 (23), 2796-2802 (2000)
MEDLINE   20309940
REFERENCE   2 (bases 1 to 3240)
AUTHORS   Isobe,M., Saitou,M. and Sugimoto,J.
TITLE   Direct Submission
JOURNAL   Submitted (29-Nov-1999) to the DDBJ/EMBL/GenBank databases.
            Masaharu Isobe, Toyama University, Materials and Biosystem
            Engineering, Faculty of Engineering; 3190 Gofuku, Toyama 930-8555,
            Japan (E-mail:isobe@eng.toyama-u.ac.jp., Tel:+81-76-445-6872,
            Fax:+81-76-445-6874)
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Query Match
Best Local Similarity   10.8%;   Score 701.2; DB 9; Length 3240;
Matches 703; Conservative   0; Mismatches   3; Indels   0; Gaps   0;

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Qy  5688  ggatcttcatgtacctgctctcttctgttgcacaccagacatagcctcctgcaggcagaa  5747
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Db  2572  GGATCTTCATGTACCTGCTCTCTTCTGTTTGCACACCAGCATAGCCTCCTTGCAGGCAGAA  2631

Qy  5748  ggcagtaggcgccctgcacactcagttctctctctcgtttctcttagttatcagtcctgtcct  5807
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Db  2632  GGCAGTAGGCGCCCTGCACACTCAGTTTCTCTCGTTTCTCTTAGTTATCAGTCCTGTCCT  2691

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Db  2752  TGTGTGCTGAGCCAGTTTCCCTGCCTGGCTGCAAGCTGTGGGTTCTTTCTCTCCTGTGGCC  2811

Qy  5928  cctcatgctgatcttctagatgccactccaaatcccctccaccaccaggatgtgtg  5987
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Db  2812  CCTCATGCTGATCTTCTAGATGCCACTCCAAATCCCCTCATACCCACCACCAGGATGTGTG  2871
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RESULT   8
LOCUS   AB035542   3240 bp   mRNA   PRI   12-DEC-2000
DEFINITION Homo sapiens TCL6f3 mRNA for T-cell leukemia/lymphoma 6 ORF105,
            T-cell leukemia/lymphoma 6 ORF72, complete cds, clone:pDG3.
ACCESSION   AB035542
VERSION   AB035542.1   GI:8176587
KEYWORDS   TCL6f3; T-cell leukemia/lymphoma 6 ORF72; TMl1
            beta ORF105.
SOURCE   Homo sapiens cell_line cDNA to mRNA, clone:pDG3.
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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RESULT  9

LOCUS       AB035340        3532 bp    mRNA              PRI        12-DEC-2000
DEFINITION  Homo sapiens TCL6f1 mRNA for T-cell leukemia/lymphoma 6 ORF141,
            T-cell leukemia/lymphoma 6 ORF72, complete cds, clone:pDG1.
ACCESSION   AB035340
VERSION     AB035340.1  GI:8176581
KEYWORDS    TML1 beta ORF72; TCL6f1; T-cell leukemia/lymphoma 6 ORF72; T-cell
            leukemia/lymphoma 6 ORF141.
SOURCE      Homo sapiens cell_line:Daudi cDNA to mRNA, clone:pDG1.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3532)
  AUTHORS   Saitou,M., Suginoto,J., Hatakeyama,T., Russo,G. and Isobe,M.
  TITLE     Identification of the TCL6 genes within the breakpoint cluster
            region on chromosome 14q32 in T-cell leukemia
  JOURNAL   Oncogene 19 (23), 2796-2802 (2000)
  MEDLINE   20305940
REFERENCE   2  (bases 1 to 3532)
  AUTHORS   Isobe,M., Saitou,M. and Sugimoto,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-NOV-1999) to the DDBJ/EMBL/GenBank databases.
            Masaharu Isobe, Toyama University, Materials and Biosystem
            Engineering, Faculty of Engineering; 3190 Gofuku, Toyama 930-8555,
            Japan (E-mail:isobe@eng.toyama-u.ac.jp., Tel:+81-76-445-6872,
            Fax:+81-76-445-6874)
FEATURES             Location/Qualifiers
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                     /clone="pDG1"
                     /cell_line="Daudi"
     gene            1768..3461
                     /gene="TCL6f1"
     CDS             1768..2193
                     /gene="TCL6f1"
                     /codon_start=1
                     /product="T-cell leukemia/lymphoma 6 ORF141"
                     /protein_id="BAA96377.1"
                     /db_xref="GI:8176582"
                     /translation="MEPRVTQRRKPLDGCMGKITGITSDILKVDHKCFKLSLPAKFPE
                     VCGSDEVFPPDDLLHVLPVAGSLQQSIDQCCLQESLCRPGLLCAHPTLLFKLHSSMK
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     CDS             3243..3461
                     /gene="TCL6f1"
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Best Local Similarity      99.6%;    Pred. No. 9.2e-159;
Matches    703;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy    5628  tccgcagcccctgctggccctgcctcttcctgttgggcttcactgtgggcccctgtc  5687
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Db    2804  TGGCTGGCCCCTGCTGGCCCTGCCTCTTCCTGTTGGGCTTCACTGTGGGCCCTGTC  2863

Qy    5868  tgtgtgtctgagccagttccccctgctgggctgcaagctgttggttcttcatcctgcc  5927
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3044  TGTGTGCTGAGCCAGTTTCCCCTGCTGGCTGCAAGCTGTGGGGTTCTTTCTTCTCGCC  3103

Qy    5928  cctcatgctgatcttctagatgccactcccaaaatcccctttcatacccaacaagatgtgtg  5987
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Db    3104  CCTCATGCTGATCTTCTAGATGCCACTCCCAAAATCCCCTTTCATACCCACCAGGATGTGTG  3163

Qy    5988  cccagcccagggcctccagcgcacccccagtcgtcagctcgtgttgattggaaactcacactcgggcagg  6047
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3164  CCCAGCCCAGGGCCTCCAGCGCACCCCCAGTCGTCGATTGGAAACTCACCATCGGGCAGG  3223

Qy    6048  cagtcggttcggtttaagagatggcattagaggggagccccagtctcggatgtggacttggatg  6107
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3224  CAGTCGGTTCGGTTTAAGAGATGGCATTAGAGGGGAGCCCCAGTCTCGGATGTGGACTTGGATG  3283

Qy    6108  ccctgtgggtatcagttctgctgacacctttggcccgaaatagatccagtgctgagcaagc  6167
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Db    3284  CCCTGTGGGTATCAGTTCTGCTGACACTTTGGCCCGAAATAGATCCAGTGCTGAGCAAGC  3343

Qy    6168  aatgtacaccgagcccatctgcacagtggggagcatggagggatgggtt  6227
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Db    3404  TGGCCTGTCGCTTCTGCTTATTCAGTCCTTCAGCTCACGGAAGGGATGCTAGTCCCTGAAG  3463

Qy    6228  tggcctgtcgcttctgcttattcagtccttcagctcacggaaggggatgctagtccctgaag  6287
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3404  TGGCCTGTCGCTTCTGCTTATTCAGTCCTTCAGCTCACGGAAGGGGATGCTAGTCCCTGAAG  3463

Qy    6288  gtgacctcacagtactggttaattaaactttattgctcactgtcca  6333
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Db    3464  GTGACCTCACAGTACTGGTTAATTAAACTTTATTGCTCACTGTCAA  3509
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RESULT  10

LOCUS       AB035341        3599 bp    mRNA              PRI        12-DEC-2000
DEFINITION  Homo sapiens TCL6f2 mRNA for T-cell leukemia/lymphoma 6 ORF141,
            T-cell leukemia/lymphoma 6 ORF72, complete cds, clone:pDG2.
ACCESSION   AB035341
VERSION     AB035341.1  GI:8176584
KEYWORDS    T-cell leukemia/lymphoma 6 ORF72; TCL6f2; T-cell leukemia/lymphoma
            6 ORF141.
SOURCE      Homo sapiens cell_line:Daudi cDNA to mRNA, clone:pDG2.
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BASE COUNT      857 a      913 c      896 g      866 t
ORIGIN
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Left column

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ORGANISM      Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1 (bases 1 to 3599)
AUTHORS       Saitou,M., Sugimoto,J., Hatakeyama,T., Russo,G. and Isobe,M.
TITLE         Identification of the TCL6 genes within the breakpoint cluster
              region on chromosome 14q32 in T-cell leukemia
JOURNAL       Oncogene 19 (23), 2796-2802 (2000)
MEDLINE       20309940
REFERENCE     2 (bases 1 to 3599)
AUTHORS       Isobe,M., Saitou,M. and Sugimoto,J.
TITLE         Direct Submission
JOURNAL       Submitted (29-NOV-1999) to the DDBJ/EMBL/GenBank databases.
              Masaharu Isobe, Toyama University, Materials and Biosystem
              Engineering, Faculty of Engineering; 3190 Gofuku, Toyama 930-8555,
              Japan (E-mail:isobe@eng.toyama-u.ac.jp., Tel:+81-76-445-6872,
              Fax:+81-76-445-6874)
FEATURES             Location/Qualifiers
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                     /map="14q32.1"
                     /clone="pDG2"
                     /cell_line="Daudi"
     gene            1768..3528
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     CDS             1768..2193
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                     /gene="TCL6f2"
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                     /db_xref="GI:8176586"
                     /translation="MALEGAQSGCGLGCPVGISSADTLARNRSSAEQAMYTGASVSPS
                     AQWGAWRDGFGLCFCLFSPSAHGRDASP"
BASE COUNT      883 a    926 c    914 g    876 t
ORIGIN

Query Match          10.8%;   Score 701.2;  DB 9;  Length 3599;
Best Local Similarity  99.6%;  Pred. No. 9.2e-159;
Matches  703;  Conservative   0;  Mismatches   3;  Indels   0;  Gaps   0;

Qy     5628 tcgcaggccctgctggcctggcctcctcctggtgtctcctcctcagtga 5687
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2871 TGGCCTGGGCCCCGTCGGCCCCTGGGCCCTGGCCCCCTCAGTGA 2930

Qy     5688 ggatcttcatgtacctgctcttctgtttgcacacccaccagatag 5747
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Db     2931 GGATCTTCATGTACCTGCTCTTCTGTTTGCACACCCAGCACGAA 2990

Qy     5748 ggcagtagggccccgcacactcagttctctctcgtttctccttagtta 5807
            ||||||||||||||||||||||||||||||||||||||||||||||||
Db     2991 GGCAGTAGGGCCCCTGCACACTCAGTTTCTCTCGTTTTCCTTAGTTA 3050

Qy     5808 gtccactcaggtctgtacttaggcaaggcaagctggcctggggtccctggc 5867
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Db     3051 GTCCCACTCAGGTCTGTACTTAGGGCAAGCTGGCCTGGGGTCCCTGGC 3110

Qy     5868 tgtgtgctgagccagtttccctgtcggtgcaagctgtgggttcttctcctc 5927
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Db     3111 TGTGTGCTGAGCCAGTTTCCCCTGCGTCGACCTGTGGGTTCTTCTCCTC 3170

Qy     5928 cctcatgctgatcttctagatgatgccactccaaatccccttcatcaccaccaggatgtgtg 5987
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Right column

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Db     3171 CCTCATGCTGATCTTCTAGATGATGCCACTCCAAATCCCCTTCATCACCACCAGGATGTGTG 3230
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Db     5988 cccagccaggcctccagcacacccccagtgcagctcgtgattggaaacctcaaccatcggcagg 6047
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Qy     3231 CCCAGGCAGGCCTCCAGCACCCCCAGTGCAGCTCGTGATTGGAAACTCAACATCGGCAG 3290

Db     6048 cagtggttcggtttaaggatggccattagaggaggagccaagtctggatgtggaacttggatg 6107
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Qy     3291 CAGTGGTTCGGTTTAAGGATGGCCATTAGAGGAGGAGCCCAGTCTGGATGTGGACTTGGATG 3350

Db     6108 ccctgtgggtatcagttctgtcgtgacacttggcccgaaatagatcagtgctgagcaagc 6167
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Qy     3351 CCCTGTGGGTATCAGTTCTGTCGTGACACTTTGGCCCGAAATAGATCCAGTGCTGAGCAAGC 3410

Db     6168 aatgtacaccggagcctcagttgagcccatctgcacagtgggggagcatgggaggggatggg 6227
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     3411 AATGTACACCGGAGCCTCAGTGAGCCCATCTGCACACAGTGGGGGAGCATGGGAGGGGATGGG 3470

Db     6228 tggcctggctgcttattcagtctcctcacggaagggatgtcagtccgtgaag 6287
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     3471 TGGCCTGGTGCTTCTGCCTTATTCAGTCTCCTTCAGCTCACACGGAAGGGATGTCAGTCCGTGAAG 3530

Qy     6288 gtgacctcacagtactggttaattaaaacttattatgctcactgtcca 6333
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Db     3531 GTGACCTCACAGTACTGGTTAATTAAAACTTTATTGCTCACTGTCAA 3576
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RESULT 11
AF137027
LOCUS       AF137027          1177 bp    mRNA            PRI       13-MAY-1999
DEFINITION  Homo sapiens syncytiotrophoblast-specific protein mRNA, complete
            cds.
ACCESSION   AF137027
VERSION     AF137027.1  GI:4809182
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1177)
AUTHORS     Jiang,B. and Mendelson,C.R.
TITLE       A syncytiotrophoblast-specific gene Syn-1 cloned from human
            syncytiotrophoblast subtracted cDNA library
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 1177)
AUTHORS     Jiang,B. and Mendelson,C.R.
TITLE       Direct Submission
JOURNAL     Submitted (24-MAR-1999) Biochemistry, UT Southwestern Medical
            Center at Dallas, 5323 Harry Hines Blvd., Dallas, Texas 75235, USA
FEATURES             Location/Qualifiers
     source          1..1177
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                     /protein_id="AAD30130.1"
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BASE COUNT      242 a    328 c    332 g    275 t
ORIGIN

Query Match          10.8%;   Score 699.8;  DB 9;  Length 1177;
Best Local Similarity  99.7%;  Pred. No. 1.9e-158;
Matches  701;  Conservative   0;  Mismatches   2;  Indels   0;  Gaps   0;

Qy     5628 tcgcaggccctgctggcctggcctcctcctggtgtctcctcctcagtga 5687
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Db 443 TGGCTGGCGCCCTGCCCTGCCCTCCTTCTGGCCTTGCTTCCTCATGCCCCTCAGTGA 502
Qy 5688 ggatcttcatgtacctgctctctgtttgcacaccagcatagcctcttgcaggcagaa 5747
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Db 503 GGATCTTCATGTACCTGCTCTCTGTTTGCACACCAGCATAGCCTCTTGCAGGCAGAA 562
Qy 5748 ggcagtagggccctgcacactcaagttctctctgtttcctgtttcct 5807
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Db 563 GGCAGTAGGGCCCCTGCACACTCAGTTTCTCTCTGCGTTTTCCTTAGTTATCAGTCCTGTCCT 622
Qy 5808 gtcccacttcaagtctgtacttagggcagctggccctgga tgggcttcactgggcgccctgtc 5867
Db 623 GTCCCACTTCAGGTCTGTACTTAGGGCAGCAGCTGGCCTTCACTGGGCCCCTGTC 682
Qy 5868 tgtgtgctgagccagtttccccctgctggcgtgggttgtcttctctcctctgtgcc 5927
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Db 683 TGTGTGCTGAGCCAGTTTCCCCTGCTGGCGTGGGTTCTTTTCTCCTCTGTGCC 742
Qy 5928 cctcatgctgatcttctagatgatgcacctcccaaatcccccttcattcaccaccaggatgtgtg 5987
Db 743 CCTCATGCTGATCTTCTAGATGATGCCACTCCCAAATCCCCTTCATTCACCACCAGGATGTGTG 802
Qy 5988 cccagccaggcctccagcacccccagtgcagctcgttgattggaaactcaccatcggccagg 6047
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Db 803 CCCAGCCAGGCCTCCAGCACCCCCAGTGCAGCTCGTTGATTGGAAACTCACCATCGGCCAGG 862
Qy 6048 caagtggttcggtttaagagatggcattagagggagggagccccagtctcggatctggatg 6107
Db 863 CAGTGGTTCGGTTTAAGAGATGGCAATTAGAGGGAGCCCCAGTCTCGGATGTGGGATCTGGATG 922
Qy 6108 ccctgtgggtatcagttctgctgctgacacttttggcccgaaataggccgaaatagatccagtgctgtgagcaagc 6167
Db 923 CCCTGTGGGTATCAGTTCTGCTGACACTTTGGCCCGAAATAGATCCAGTGCTGCTGAGCAAGC 982
Qy 6168 aatgtacaccggaacctcaagtgagcccatctgcacagtgggggagccatggaagggatgggtt 6227
Db 983 AATGTACACCGGAGCCTCAGTGAGCCCATCTGCACAGTGGGGGAGCCATGGAAGGGATGGGTT 1042
Qy 6228 tggcctgtggtctgcttattcagtcctcagctcacggaaggggatgctagtcgtgaag 6287
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Db 1043 TGGCCTGTGGTCTTCTGCTTATTCAGTCCTTCAGCTCACGGAAGGGGATGCTAGTCGGTGAAG 1102
Qy 6288 gtgacctcacagtactggttaattaaactttattgctccactgt 6330
Db 1103 GTGACCTCACAGTACTGGTTAATTAAACTTTATTGCTCACTGT 1145

RESULT 12

LOCUS   AB025272S2   753 bp   DNA   PRI   14-APR-2000
DEFINITION   Homo sapiens gene for TCl1 / MTCP1-like 1, exon 2.
ACCESSION   AB025273
VERSION   AB025273.1 GI:5478617
KEYWORDS   TMl1; TCl1 / MTCP1-like 1.
SEGMENT   2 of 3
SOURCE   Homo sapiens
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (sites)
  AUTHORS   Sugimoto,J., Hatakeyama,T., Narducci,M.G., Russo,G. and Isobe,M.
  TITLE   Identification of the TCl1/MTCP1-like 1 (TMl1) gene from the region
             next to the TCl1 locus
  JOURNAL   Cancer Res. 59 (10), 2313-2317 (1999)
  MEDLINE   99274532
REFERENCE   2 (bases 1 to 753)
  AUTHORS   Isobe,M., Sugimoto,J. and Hatakeyama,T.
  TITLE   Direct Submission
  JOURNAL   Submitted (24-MAR-1999) to the DDBJ/EMBL/GenBank databases.
             Masaharu Isobe, Toyama University, Faculty of Engineering; Gofuku
             3160, Toyama, Toyama 930-8555, Japan
             (E-mail:isobe@eng.toyama-u.ac.jp, Tel:+81-76-445-6872,
             Fax:+81-76-445-6874)

FEATURES   Location/Qualifiers
     source   1..753
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                     /clone="p20-7D4"
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                     /map="14q32.1"
     exon   223..393
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ORIGIN

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Matches 645; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4324 gaattctgaaacatttacctctcgaccctggcagccaacctgccattgcttgtgtgcagc 4383
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Db 108 GAATTCTGAAAACATTTACCTCTCGACCCTGGCAGCCAACCTGCCATTGCTTGTGTGCAGC 167
Qy 4384 ccagttggcaggggaaccctatccatgatcatgattgccgcctctttctgtccttcagtatga 4443
Db 168 CCAGTTGGCAGGGAACCCTATCCATGATGATTGCCGCCTCTTTCTGTCCCTTCAGTATGA 227
Qy 4444 accagcatcacagtgcacttgtggcagatggcagtgcatcaccgggagctactcctctc 4503
Db 228 ACCCAGCATCACAGTGCACTTGTGGCAGATGGCAGTGCATCACCGGGAGCTACTCCCTC 287
Qy 4504 cggccagatgcccctctcctcccagctgcccgccgtgtgggcagctctacaccccgggagggaagta 4563
Db 288 CGGCCAGATGCCCTCTCCCAGCTGCCCGCCGTGTGGGCAGCTCTACCCCGGGAGCTACTCCCTC 347
Qy 4564 ccggagcacgggattccagttctcggggaaatagcagaccatggccaggcaagtgtgtggtg 4623
Db 348 CCGGACGAGCGGGATTCCAGTTTCTCGGGAAATAGCACCATGGCCAGGCAAGTGTGTGGTG 407
Qy 4624 gttctaagtgtaaaagcgacaggtggccccctggtgactgcgtggccctctctcctgtgc 4683
Db 408 GTTCTAGGTGAAAGCGACAGGTGGCCCCTGGTGACTGCGTGGCCCTCTCTCCTGTGC 467
Qy 4684 ccctggcccccctggggttcttgtctgtcctcttcctgttgcttcaagtctttcccttcaagg 4743
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Qy 4744 aggcctgagtgtgtgttgggtgggatcggtgcatgagttcccatgtgggatgcaggagagt 4803
Db 528 AGGCCTGAGTGTGTGTTGGGTGGGATCGGTGCATGAGTTCCCATGTGGGATGCAGGCAGAGT 587
Qy 4804 gggtgaggagggaggggttgcctccctgggctaggggaaatccataagctggagttccca 4863
Db 588 GGGTGAGGGAGGGAGGGGTTGCCTTCCCTGGGCTAGGGAAATCCATAAGCTGGAGTTCCCA 647
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Qy 4924 ggaagagcatctcccagaggttctgaatggctgctccctcctgca 4969
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Db 708 GGAAGAGCACTCTCCCAGAGGTTCCTGAATGGCCTGCTCCCTCCTCGCA 753

RESULT 13

LOCUS   AB025272S1   627 bp   DNA   PRI   14-APR-2000
DEFINITION   Homo sapiens TMl1 gene for TCl1 / MTCP1-like 1, exon 1, partial
             sequence.
ACCESSION   AB025272
VERSION   AB025272.1 GI:5478616

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KEYWORDS    TML1; TCL1 / MTCP1-like 1.
SEGMENT     1 of 3
SOURCE      Homo sapiens adult DNA, clone:p20-7H1.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (sites)
AUTHORS     Suginoto,J., Hatakeyama,T., Narducci,M.G., Russo,G. and Isobe,M.
TITLE       Identification of the TCL1/MTCP1-like 1 (TML1) gene from the region
            next to the TCL1 locus
JOURNAL     Cancer Res. 59 (10), 2313-2317 (1999)
MEDLINE     99274532
REFERENCE   2 (bases 1 to 627)
AUTHORS     Isobe,M., Suginoto,J. and Hatakeyama,T.
TITLE       Direct Submission
JOURNAL     Submitted (24-MAR-1999) to the DDBJ/EMBL/GenBank databases.
            Masaharu Isobe, Toyama University, Faculty of Engineering; Gofuku
            3160, Toyama, Toyama 930-8555, Japan
            (E-mail:isobe@eng.toyama-u.ac.jp. Tel:+81-76-445-6872,
            Fax:+81-76-445-6874)
FEATURES             Location/Qualifiers
     source          1..627
                     /organism="Homo sapiens"
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                     /chromosome="14"
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                     /dev_stage="adult"
                     /map="14q32.1"
     exon            <119..310
                     /gene="TML1"
                     /note="There is a complete cds information in AB025274."
                     /product="TCL1 / MTCP1-like 1"
                     /number=1
BASE COUNT      113 a    195 c    210 g    109 t
ORIGIN

Query Match      8.8%;  Score 570.4;  DB 9;  Length 627;
Best Local Similarity   97.8%;  Pred. No. 3.4e-127;
Matches  610;  Conservative  0;  Mismatches  11;  Indels  3;  Gaps  3;

Qy    18 ctccccgactggcacccgcccccactgcgcccccgccggcccgggcccca 77
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Qy    78 cccacgccggagctgctccatttaaggagatgcgcgagctgacacgtgtggac 137
         |||||||||||||||||||||||||||||||||||||    |||| |||||||
Db    60 CCCACGCCGGAGCTGCTCCATTTAAGGAGATGCCCAG-TGGAAAGCTACACGTGTGAGC 118

Qy   138 ctagagggggtcccggttgcagactgcatggccgctccgaagcttcttgtgtgtctaggg 197
         |||||| |||||||||||||||||||| ||||||| |||||||||||| ||| |||||||
Db   119 CTAGAGGCGGGGTCCCGGTTGCAGACTTGCCATGGCCTCCCGAAAGCTTCTGTGCGGTCTAGGG 178

Qy   198 gtgccccctggcgcctctggtggatccagaggggcctgggcatctacagatgaggaggggagg 257
         |||||||||||| ||| ||| ||||||| |||||||| ||||||||| || |||||||||||
Db   179 GTGCCCCCTGGCCGGTCTGTGGAATCCACAGAGGCCTGGCCATCTACGAACATGAGGAGGGGAGA 238

Qy   258 aacctggggtgactggtggttcggtgcgggttcaatacccctcccgtaggggaatggccaggggcctcc 317
         | |||| |||||||||||| |||| |   ||||||| ||||| |||| |||||||| ||||| |||||
Db   239 ACTGGGTGACTGGTGGTCGGTTCAATCCCTCGCGTTAGGGAATGGGCCAGGGCCTCC 298

Qy   318 cagggcagcagaagtgagtcctgggcacgagggggagggctgtggggaggggctgcgcactgac 377
         |||||||||||| |||||||||||||||||||| |||||| |||   |||||| |||||||||
Db   299 CAGGGCAGCAGAGTGAGTCCTGGGCACGAGGGGAGGGCTTGCCACTGAC 358

Qy   378 ccctgcgccgtgtggaaccggcggtggggtcaggggggtcccgttctcacccgcactggaaa 437
         |||||||||||||||||||| ||||||| |||| |||||  ||||||||||||||||||||
Db   359 CCCTGCGCCGTGTGGAACCCGGTGGGGGGTCAGAGGGGGCGTTCTCACCCGCACTGGAAA 418

Qy   438 acttcactttctgtgcaggtctaggagcggcagcagcaatgtccatgcccagccctgcccagga 497
         ||| |||| | |||||||| |||||||| ||| |||| ||||||||||||||||||||||||||
Db   419 ACTCACTTCGTGTGCAGGGTCTAGGAGCGCAGCCAGCCAATGTCCATGCCCAGCCCTGCCCCAGGA 478
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```
RESULT 14
AC016603
LOCUS       AC016603   110879 bp    DNA                 PRI       20-JUL-2001
DEFINITION  Homo sapiens chromosome 5 clone CTD-2132G23, complete sequence.
ACCESSION   AC016603
VERSION     AC016603.6  GI:14971185
KEYWORDS    HTG.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 110879)
AUTHORS     DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE       Direct Submission
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 110879)
AUTHORS     DOE Joint Genome Institute.
TITLE       Direct Submission
JOURNAL     Submitted (04-DEC-1999) Production Sequencing Facility, DOE Joint
            Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE   3 (bases 1 to 110879)
AUTHORS     DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE       Direct Submission
JOURNAL     Submitted (20-JUL-2001) DOE Joint Genome Institute, 2800 Mitchell
            Drive, Walnut Creek, CA 94598, USA
COMMENT     On Jul 20, 2001 this sequence version replaced gi:7711572.
            Draft Sequence Produced by DOE Joint Genome Institute
            www.jgi.doe.gov
            Finishing Completed at Stanford Human Genome Center
            www-shgc.stanford.edu
            Quality: Phrap Quality >=40 99.9% of Sequence;
            Estimated Total Number of Errors is 0.1.
            STS Content:
            WI-31186 G24491.
FEATURES             Location/Qualifiers
     source          1..110879
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="5"
                     /clone="CTD-2132G23"
BASE COUNT    33303 a   18836 c   20019 g   37821 t
ORIGIN

Query Match      7.8%;  Score 506;  DB 9;  Length 110879;
Best Local Similarity   87.1%;  Pred. No. 1.4e-111;
Matches  603;  Conservative  0;  Mismatches  80;  Indels  9;  Gaps  4;

Qy   498 acacccccgtaaagggaccacaggcacaagcttatccacaatgagataaatgtggttcctgc 557
         |||||||||||||||||||||||| |||||| |||||||||| |||||| |||||||||||
Db   479 ACACCCCCGTAAAGGGACCACAGCCACAGGCAAAGCTTATCCACATGAGATAATGTGGTTCCTGC 538

Qy   558 gtggtgaagccgaggctaaggtagctcaggggcttagtgcaattcccagttgcctgctgggga 617
         ||||||||||||||||||||| |||||||||||||||||| |||||||||| |||||| ||||
Db   539 GTGGTGAAGCCGAGGCTAAGTTAGCTCAGGGGCTTAGTGCCATTCCCAGTGCCTGCTGTGGGA 598

Qy   618 aggcccacaaatgggcagctatt 641
         |||||||| ||||||| |||||||
Db   599 AGGCCCAC-AATGGGGCAGCTATT 621
```

```
Qy  5646 ctgcctcttctggcctggttgtctctcatcgtccccctcaagtgaggatcttcatgtacctgc 5705
         ||| || ||||||||| |  | |  || | ||||||||||||||||| ||||| ||||||| ||
Db   376 CTGACTCCTCTGGCCTCCATGTTCTTCTTCGGGCCCCCTCAGTGAGGAATCTTTTGTGTACTTGC 435

Qy  5706 tcttctgttgcaacaccagatagcctccttgcaggcagaaggcagtagggccctgca 5765
         |||||||||||||| |||| |||||||  ||||||||| ||| || ||||||||| |||
Db   436 TATTCCGTTTGCACACCACCAGCGTGGCCTTTCTGCAGGCAGGAGGACGAGCCAGTGGGGCCCCTGCA 495

Qy  5766 cacctaagtttctctcgttttccttagttatcaagtcctgtcctgtccactcaggtctgta 5825
         |||| ||| ||||||| |||| ||| |||||||| ||||| |  |||| |||||||| ||| |
Db   496 CACTCAGCTTCTCTCATTTCTTCACTTATCAGTCTTGTTTGTCCGTTCCACTCAGATCTACA 555
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```
RESULT 15
LOCUS       AC010356/c
LOCUS       AC010356   114438 bp   DNA   HTG   05-MAY-2000
DEFINITION  Homo sapiens chromosome 5 clone CTD-2028C21, WORKING DRAFT
            SEQUENCE, 10 unordered pieces.
ACCESSION   AC010356
VERSION     AC010356.4  GI:7710750
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 114438)
AUTHORS     DOE Joint Genome Institute.
TITLE       Sequencing of Human Chromosome 5
JOURNAL     Unpublished
REFERENCE   2  (bases 1 to 114438)
AUTHORS     DOE Joint Genome Institute.
TITLE       Direct Submission
JOURNAL     Submitted (15-SEP-1999) Production Sequencing Facility, DOE Joint
            Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT     On May 5, 2000 this sequence version replaced gi:7341483.
            -----Genome Center.
            Center: Joint Genome Institute
            Center Code: JGI
            Web site: http://www.jgi.doe.gov
            -----
            Project Information
            Center Project Name: 638370
            Center clone name: CITB-H1_2028C21
            -----
            Summary Statistics
            Consensus quality:  105028 bases at least Q40
            Consensus quality:  110833 bases at least Q30
            Consensus quality:  111997 bases at least Q20
            Estimated insert size: 123000; pulse field gel estimation
            Estimated insert size: 113538; sum-of-contigs estimation
            Quality coverage: 4.61 in Q20 bases; pulse field gel estimation
            Quality coverage: 4.99 in Q20 bases; sum-of-contigs estimation.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 10 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
FEATURES             Location/Qualifiers
     source          1..114438
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="5"
                     /clone="CTD-2028C21"
                     /clone_lib="CalTech human BAC library D"
     *        1      2455: contig of 2455 bp in length
     *     2456      2555: gap of unknown length
     *     2556      5533: contig of 2978 bp in length
     *     5534      5633: gap of unknown length
     *     5634      9013: contig of 3380 bp in length
     *     9014      9113: gap of unknown length
     *     9114     13014: contig of 3901 bp in length
     *    13015     13114: gap of unknown length
     *    13115     19656: contig of 6542 bp in length
     *    19657     19756: gap of unknown length
     *    19757     25844: contig of 6088 bp in length
     *    25845     25944: gap of unknown length
     *    25945     37665: contig of 11721 bp in length
     *    37666     37765: gap of unknown length
     *    37766     61723: contig of 23958 bp in length
     *    61724     61823: gap of unknown length
     *    61824     86508: contig of 24685 bp in length
     *    86509     86608: gap of unknown length
     *    86609    114438: contig of 27830 bp in length.
BASE COUNT    36135 a  22103 c  21741 g  33555 t   904 others
ORIGIN

Query Match              7.8%;    Score 506;  DB 2;   Length 114438;
Best Local Similarity   87.1%;    Pred. No. 1.4e-111;
Matches   603; Conservative   0; Mismatches   80;  Indels   9;  Gaps   4;

Qy  5646 ctgcctcttctggcctggtgtctcctcatgccccctccagtgaggatcttcatgtacctgc 5705
         ||| |||| ||||||||||| |||||| |||| ||||||||||||||||| ||| |||| ||
Db 74566 CTGACTCTCTGCCCTCATGTCTCTTCGGGCCCCTCAGTGAGGATCTTTGTGTPACTTGC 74507

Qy  5706 tcttctgtttgcaacaccccagcatagcctcctgcaggcagaagagcagtaggagccctgca 5765
         ||||||||||| | |||||||||||  |||||||||||||||||||||||||||| |||||||
Db 74506 TATTCCGTTTGCACACCCAGCGTGGCCTCCTTGCAGGACAGAGGCACTGGGGCCCCTGCC 74447

Qy  5766 cactcagttctctcgttttcctcttagttatcagtcctgtcctgtcccactcaggtctgta 5825
         ||||||| |||||||| |||||| |||||||| |||||||||||||||||||||||||| |||
Db 74446 CACTCAGCTTCTCACATTTTCTCACTTATCAGTCTTGTCCTGTCGTTTTCACTCAGATCTACA 74387

Qy  5826 cttagggcaagctggctggatggcttcact-gggccctgtctgttgctgagccagtt 5884
         ||||||||||| ||||||||||||||||||| |||||||| ||| |||||||||||||
Db 74386 CTGAGGGCAGTTGGCCTGGATGGGCTTCACTCAGGGCCGTCTGTCGACTGGGCCGTT 74327

Qy  5885 tccctgctgctgcaagctgtgggttc--tttctcctctgtgccctcatgctgatctt 5942
         ||||||||||||||||||| |||||||  |||||||||||||||||||||||||| ||
Db 74326 TCCCCTGCTGCTGCAAGCCATGGGTGTTCTTTTTTCTCCTCTCTCTGCCCTCATGCTGACTT 74267

Qy  5943 ctagatgccactcccaaatccccctt---cataccaccacaggatgtgtgccagccagg 5997
         ||||| || |||||||||| |||| ||   |||||||||||||| |||||||||||||||
Db 74266 CTAGATGCCCACTCCCAAATCCCCTTCACTCACTCACCACCAGGCTTCATGCCCACCAGG 74207

Qy  5998 cctccagcaccccccagtgcagctcgtgattggaaactcaccacatcggacagcaggttcg 6057
         |||||||||||||||||| |||||||||||||||||| ||||||||||| ||||||||||||
Db 74206 CCTCCTGGCTGCGCACCTTCAGTGCACATGATTGGGGAACTCACCATCACCAGGCTTCATGCCCACCAGG 74147
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(RESULT 15 alignment — Query vs Db)

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Qy  5826 cttagggcaagctggctggatggcttcact-gggccctgtctgttgctgagccagtt 5884
          556 CTGAGGGCAGTTGGCCTGGATGGGCTTCACTCAGGGCCGTCTGTCGACTGGGCCGTT 615
Qy  5885 tccctgctgctgcaagctgtgggttc--tttctcctctgtgccctcatgctgatctt 5942
          616 TCCCCTGCTGCTGCAAGCCATGGGTGTTCTTTTTTCTCCTCTCTCTGCCCTCATGCTGACTT 675
Qy  5943 ctagatgccactcccaaatccccctt---cataccaccacaggatgtgtgccagccagg 5997
          676 CTAGATGCCCACTCCCAAATCCCCTTCACTCACTCACCACCAGGCTTCATGCCCACCAGG 735
Qy  5998 cctccagcaccccccagtgcagctcgtgattggaaactcaccacatcggacagcaggttcg 6057
          736 CCTCCTGGCTGCGCACCTTCAGTGCACATGATTGGGGAACTCACCATCACCAGGCTTCATGTGGCTCG 795
Qy  6058 gtttaagagagatggcattagaggagggagccaagtctggatgtggactggatgcctgtgggt 6117
          796 GTTTAAGAGAGAGGGCGCGAGAGGAGGGAGAACTGGGTCTGGATGTGGACTTGGATGCCCTGTGGGT 855
Qy  6118 atcagttctgctgacacttttggcccgaaataagatccagtgctgagcaagcaatgtacacc 6177
          856 ATCAGTTCTGTCGACACTTTGGCTGAAATAGATAAAGTGCTGAGCAAGCAGTGTATTGCT 915
Qy  6178 ggagcctcagtgagcccatctgcacagtgggagcatggaggatgggtttggcctgtgtgc 6237
          916 GGAGCCTCAGTAAGTCCATCTGCACAGTGGGCAGAGCCATGGGGCCCTGTTTATGC 975
Qy  6238 tcctgcttattcagtcctcacggaaaggatgagctagtcgtcgaagtgacctcac 6297
          976 TTCTGCTTGTTCAGTCTTTCACTGCTCACAGCA-GGATCGTAATCCATGAAGGTGCACTCGC 1034
Qy  6298 agtactggttaattaaacttattgctcactg 6329
         1035 AGTACTAGTTGGTTAATTAAGCTTTTATTGCTCACTG 1066
```

```
Qy    6058  gtttaagaagatggcattagaggggagcccagtgtctggatgtggaacttggattgccctgtgggt  6117
            ||||||||||| |||     ||||||||| |-    ||||||||||||||||||||||||||||||||
Db   74146  GTTTAAGAGAGGGGCCCGCAAGAGGGAACTGGGGTCTGGATGTGGAACTTGGAATGCCCTGTGGGT  74087

Qy    6118  atcagttcttgctgacaacttttggcccqgaaataagatccagttgctgagcaagccaatgtacacc  6177
            ||||||||||||||||||||| |||||||||||||    ||||||| |||||||| |||||| ||-
Db   74086  ATCAGTTCTTCGCTGACACTTTGGCCTGAAAATAAGATTAAAAGTGCTGAGCAAGCAGTGTATGCT  74027

Qy    6178  ggagcctcagtgagcccaatctgtgcacagtggggagcatggggatgggtttggcctgtgc  6237
            |||||||||| ||||||||||||||||||||||||||| | ||||||||||| |||||-|-|
Db   74026  GGAGCCTCAGTAAGTCCATTCTGCACAGTGGGGAGCCGTGGAGGGATGGGTTTGGCTTATGC  73967

Qy    6238  ttctgcttattcagtccttcagcctcacggaagggatgctagtccgtgaaggtgacctcac  6297
            |||||||| |||||||||||||| ||||||||||||||| - |||||||||||||||||||||-
Db   73966  TTCTGCTTGTTCAGTCTTTCAGCTCACAGCCA-GGATGCTAATCCATGAAGGTGACCTCGC  73908

Qy    6298  agtactggttaattaaacttttattgctcactg  6329
            ||||||||| |||||||||||||||||||||||-
Db   73907  AGTACTGGTTAATTAAGCTTTATTGCTCACTG  73876
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Search completed: November 29, 2001, 09:18:45
Job time: 18766 sec